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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

July 13, 2006, 13:40:22; Search time 194 Seconds (without alignments) 723.533 Million cell updates/sec е ::

US-10-510-941-2 1542 1 LETLLELRONOSKTIRGKKII......KSLEDRFLEITADKEEAQHV 307 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2589679 segs, 457216429 residues Searched:

2589679 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp2006s:* Geneseq_8:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Adn97355 B. lichen	Ads27585 Bacterial		Abu32480 Protein e	Abb48180 Listeria		Abu44428 Protein e	Ads28089 Bacterial	Adn27185 Bacterial	Adn48041 Thermococ	Ads41933 Bacterial	Adn18644 Bacterial	Adn18683 Bacterial	Adn46530 Thermococ	Ads27537 Bacterial	Aee95518 E. faecal	Adn46418 Thermococ	Aab96628 Putative	Ads43172 Bacterial	Abu25506 Protein e	Adc97283 E. faeciu	Aab96710 Putative	Abp26280 Streptoco
a	ADN97355	ADS27585	ABB47477	ABU32480	ABB48180	ADG32114	ABU44428	ADS28089	ADN27185	ADN48041	ADS41933	ADN18644	ADN18683	ADN46530	ADS27537	AEE95518	ADN46418	AAB96628	ADS43172	ABU25506	ADC97283	AAB96710	ABP26280
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* Query Match Length DB	307	310	301	301	306	309	302	306	299	311	306	308	318	309	221	308	322	305	305	306	310	325	300
Query Match	100.0	47.9	47.6	47.6	41.4	41.4	34.8	34.7	33.5	32.5	32.0	32.0	31.9	31.8	31.5	31.4	30.8	30.7	30.7	29.5	29.2	29.3	29.5
Score	1542	738.5	734	734	639	638	536	535.5	216	501	493	493	491.5	490	485	484.5	474.5	473	473	455.5	455.5	451.5	451
Result No.	1	7	m	4	2	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

Abu26098 Protein e Adb11670 Alloiococ Adn46668 Thermococ Abp26335 Streptoco		Abg72543 Streptoco Adu80820 MufF, SEQ Adu829173 Bacterial Adu47270 Thermococ Abu24420 Protein e	Ads29082 Bacterial Ads29721 Bacterial Ads2132 Bacterial Ads2125 E. faeciu Ad92767 C glutami Ad146278 Thermococ Ad87622 Bacterial Ad118549 Bacterial
6 ABU26098 6 ADB11670 8 ADN46668 5 ABP26335	8 ADV88530 8 ADV91939 8 ADV79783 8 ADS22213 5 ABB09645	6 ABG72543 8 ADG80820 8 ADS29173 8 ADM47270 6 ABU24420	8 ADS29082 8 ADS29721 7 ADS2132 4 AAC94125 8 ADN462767 8 ADS27622 8 ADN18549
285 377 328 300	300 300 311 233	233 233 305 310	300 300 300 300 300 300 300 300 300 300
29.0 28.8 28.7	28.7 28.7 28.7 28.4	28.5 28.5 28.5 28.5 28.5	28.0 27.9 27.8 27.8 27.6
447.5 447.5 444 442	4 4 4 4 4 4 4 4 4 4 2 2 4 8 8 6 8 8	436 436 435.5 434.5	431.5 431.5 430.5 428.5 428.5 424.5
24 25 27	33 3 5 8 8 3 5 8 8 9 5 8 9 5 9 5 9 5 9 5 9 5 9 5 9 5	3 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	8 6 6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

antibiotic synthesis; proteolytic; protease. Ź ADN97355 standard; protein; 307 (first entry) 01-JUL-2004 ADN97355; RESULT 1 ADN9735

B. licheniformis antibiotic synthesis related protein SEQ ID NO:2.

Bacillus licheniformis.

WO2003087142-A2. 23-OCT-2003.

25-MAR-2003; 2003WO-DK000199. 10-APR-2002; 2002DK-00000532.

(NOVO) NOVOZYMES AS.

Rasmussen MD, Olsen PB, Clausen IG; Andersen JT, Jorgensen ST, WPI; 2003-833704/77. N-PSDB; ADN97354. New Bacillus licheniformis mutant host cell that is mutated in one or more gene(s) encoding one or more polypeptide(s) having proteolytic activity, useful for producing, isolating and/or purifying at least one product of interest.

Disclosure; SEQ ID NO 2; 100pp; English.

The invention relates to a novel Bacillus licheniformis mutant host cell derived from a parent B. licheniformis host cell, where the mutant host cell is mutated in one or more gene(s) encoding one or more polypeptide(s) having proteolytic activity that is at least 80% identical to any of the 22 amino acid sequences fully defined in the specification, where the mutant host cell expresses at least 5% less of one or more polypeptide(s) having a proteolyric activity than the parent host cell, when they are cultivated under comparate conditions. The host cell is useful for producing at least one product of interest, and for isolating or purifying the product of interest. The present sequence represents an

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useful for producing plants with improved properties
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                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 48.5'
Matches 147; Conservative
  source,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308
                                                                                                                                                                                                                                                                 Sequence 310 AA;
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 microbial
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                                                                                                                                                                                                                                                                                                                                                                                          Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                      GLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR
                                                                                                                                                           121 GLKARINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR
                                                                                                                                                                                  EKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTR
                                                                                                                                                                                              EAAAFRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEITAD
                                                                          LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGE
                                                                                                            IAVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELV
                                                       Gaps
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                                      Length 307;
  antibiotic synthesis related polypeptide of the invention
                                                      Indels
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                                     Query Match 100.0%; Score 1542; DB 7; Best Local Similarity 100.0%; Pred. No. 3e-130; Matches 307; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen X,
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                                                                                                                                                                                                                                                                                                                                                                            Bacterial polypeptide #16618,
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SLATER S C.
CHEN X.
                                                                                                                                                                                                                                                                         KEEAQHV 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-061375/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hinkle GJ,
                     Sequence 307 AA;
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(CHEN/)
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the invention is a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant having an improved property. The plant is a crop plant canner as maize or soybean. The method of producing a transformed plant the recombinant DNA construct and a method of producing a crop plant canner as maize or soybean. The method of producing a transformed plant the comprision improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant where the polynucleotide or polypeptide is useful for improving plant with the comproved plant properties, e.g. improved cold, heat or drought tolerance, improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved plant growth regulators, increased rate of content, improved plant growth and development under at least one stress production improved lignin production or improved galactomannan condition, improved lignin production or improved galactomannan condition, improved lignin production or improved galactomannan condition. Nate sequence repersents a bacterial polypeptide used in the scope of the invention. Nate: The sequence data for this patent did not form part of the printed specification but was obtained in electronic correct form part of the printed specification but was obtained in electronic correct form part of the printed specification but was obtained.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ë,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 MITILSVRDLKKVIGKKTLVENISFDVKQGEVFGFLGFNGAGKTITIRMLVGLIKATEGT
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                                                                            relates to a recombinant DNA construct comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٠<u>,</u>
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48.5%; Pred. No. 7.8e-58;
ive 66; Mismatches 81;
Claim 1; SEQ ID NO 16618; 122pp; English.
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ABU32480 standard; protein; 301 AA

RESULT 4 ABU32480 ABU32480;

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The present invention relates to the genome sequence of Listeria monocytogenes ED-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic collymorphisms and other genomes. The present sequence is a protein canceded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and constitution to the genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication of sequence and proteins encoded by it are also useful for selecting compositions for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this monocytogenes and related organisms. Note: The sequence data for this in electronic format directly from WIPO at it electronic town and the printed specification, but was obtained in electronic format directly from WIPO at the printed part of the printed specification, but was obtained in a sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related
                                                                                                                                                                                                                                                                Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihl H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P). Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Varquez-Boland JA, Domaniels G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Charbat A, Durant L, Perez-Diaz J, Baquero F, Garcia B, Portillo F, Gomez-Lopez N, Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; SEQ ID NO 182; 192pp; French.
                                                                                                                                 11-APR-2001; 2001WO-FR001118.
                                                                                                                                                                             11-APR-2000; 2000FR-00004629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 49.8% Matches 149; Conservative
Listeria monocytogenes
                                                                                                                                                                                                                      (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-010914/01.
                                                                                                                                                                                                                                                                                                                                                                                                                             Voss H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 301 AA;
                                           WO200177335-A2.
                                                                                                                                                                                                                                                              Buchrieser C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides.
                                                                                       18-OCT-2001
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                                                                                                                                                                       LKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTRE 181
                                                                                                                                                                                     KGMAVIVSSHLLSEMELMCDRIAIIQNGK-LRDIQHVHGPARDEKKRYYIQADDTQALTR 240
                                                                                     62
                                                                                                                                                                                                                                                                                                   EAAAF-RKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEIT 298
                                                                         62 AVGUSUKENFEKAARHIGAIVENPELYKFLIGYQNLQQYARMIKGUTKKKIDEIVELVG
                                                                                                                               2 ETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEI
                              8;
47.6%; Score 734; DB 5; Length 301; 49.8%; Pred. No. 1.9e-57;
                             81; Indels
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Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
                                                                                                                                                 Ohlsen KL,
Forsyth RA,
                            Protein encoded by Prokaryotic essential gene #18007.
                                                                                                                                                 Haselbeck R,
                                                                                                                                                       Yamamoto R,
                                                                                                                                                 Malone C,
                                                                                                                                                       Carr GJ,
                                                                                                 21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                       21-MAR-2002; 2002WO-US009107
                 (first entry)
                                                                                                                                      (ELIT-) ELITRA PHARM INC.
                                                    Listeria monocytogenes.
                                                                                                                                                 Zamudio C,
Trawick JD,
                                                                                                                                                                   WPI; 2003-029926/02.
                                                                                                                                                                         N-PSDB; ACA36350
                                                                WO200277183-A2.
                 19-JUN-2003
                                                                           03-OCT-2002.
                                                                                                                                                 Wang L,
Wall D,
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New antiaense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 60404; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid nucleic acid, (2) a host cell containing the vector; (3) an isolated cuding a polypeptide whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding collideration or the activity of agene in an operon required for proliferation or the activity of agene in an operon required for proliferation or that has an activity against a biological pathway crequired for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological correquired for proliferation. Or that inhibits of the proliferation or the compound that inhibits spene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or organism acts; (9) manufacturing in a culture or collection of the strains; or (13) identifying the target of a compound that inhibits the constraint or the strains; or (13) identifying the target of a compound that inhibits the constraint or a pencenning proteins or screening for homologous nucleic acids required constraint and antisense nucleic acids are useful for the collidar proliferation of sendidate and each of the each of the capanism. The antisense nucleic acids are useful for the collidar proliferation of an organism. The antisense modeled acids are useful and antisense modeled acids are useful and antisense modeled acids acids required for the collidar proliferation of an organism. drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent din not form part of the printed specification, but was obtained in electronic format directly from WIPO at they printed specification, but was obtained ftp.wipo.int/pub/published_pct_sequences

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monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 AVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMT-KGVTKKKIDEIVELV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 EKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 VLATLPVKLVAQNEDLFKIEVAHEDVHLIARALIQANIDLLEMVPLQASLEERFLELT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAAAFRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEIT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 host cell; production yield; shelf life; product stability;
                                                                                                                                                                                                                                                                                                                                                                          41.4%; Score 639; DB 5; Length 306; 45.3%; Pred. No. 7.1e-49; ive 57; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutant B_licheniformis secreted polypeptide SeqID 84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rasmussen MD,
                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADG32114 standard; protein; 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-APR-2002; 2002DK-00000534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003; 2003WO-DK000198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andersen JT, Jorgensen ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 45.3
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             secreted; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-053045/05.
N-PSDB; ADG32113.
                                                                                                                                                                                                                                                                                                                                          Sequence 306 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003093453-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG32114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           purity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
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                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                           63 LIGGKDIRKNFTEAMRGLGSIVENPEFYTFLTGQENLAYFARMDSSIKKERIQEVTELVG 122
                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                            KGMAVIVSSHLLSEMELMCDRIAIIQNGK-LRDIQHVHGPARDEKKRYYIQADDTQALTR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAAAF-RKVKVDEAEGGIELSIQKDEVPDLIKHLIDSGVRLYEVKAVNKSLEDRFLEIT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dehoux P;
Cossart P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buchrieser C, Frangeul L, Couve B, Rusniok C, Fsihi H, Dehoux P, Dussurget O, Checuani F, Nedjari H, Glaser P, Kunst F, Cossart P Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Chakrin A, Amend B, Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez M, Maduento E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                62 AVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELVG
                                                                                                                                                                                                                                                                                                                       LKNRINDKVKTYSLGMRORLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTRE
                                                                                                                                                         2 ETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEI
                                                                                                                   Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibacterial; gene thexapy; vaccine; biosynthesis; biodegradation;
vitamin B12; bacterial infection; disease.
                                                                                                                 8
                                                                        Length 301;
                                                                                                                 Indels
                                                                                                                   81;
                                                                        47.6%; Score 734; DB 6;
49.8%; Pred. No. 1.9e-57;
tive 61; Mismatches 81,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; SEQ ID NO 885; 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Listeria monocytogenes protein #884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB48180 standard; protein; 306
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Perez-Diaz J, Baquero F, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-APR-2001; 2001WO-FR001118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-2000; 2000FR-00004629
                                                                                         Local Similarity 49.8%
nes 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-010914/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vовв Н;
                                    Sequence 301 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200177335-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-OCT-2001.
                                                                                                                 Matches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                              183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB48180;
                                                                                                                                                                                                                                                                                                                         122
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                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Кове М,
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Clausen IG;

Olsen PB,

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This invention relates to a novel Bacillus licheniformis (B. licheniformis) mutant host cell derived from a parent B. licheniformis host cell that is mutated in genes encoding secreted polypeptides.

Specifically, it refers to the generation of an improved Bacillus host that reduces the need for product purification caused by contaminant secreted native polypeptides in the culture medium. Accordingly, the present invention describes reducing the expression of these native protectins (e.g. proteclytic enzymes nutrient uptake factors and signal molecules), which in turn makes it easier to purify the heterologous product of interest and therefore improving the production process. Further benefits of a mutated host cell include an increase in total product in yield and a longevity of Shelf life attributable to improved product stability and purity. This polypeptide is a mutant B.
                          one
                     New mutant Bacillus licheniformis host cell secreting 5 % less of more secreted polypeptides than the parent host cell, useful for producing a product of interest e.g. polypeptides, amino acids or
                                                                                                                                              Claim 1; SEQ ID NO 84; 422pp; English.
                                                                                                   carbohydrates.
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Sequence 309 AA;

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GVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELVGLKN 124
                                                                                                                                                           RINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKGM 184
                                                                                                                                                                                                                               185 AVIVSSHLLSEMELMCDRIALIQNGKLRDIQHVHGPARD-EKKRYYI----QADDTQALT 239
                                                                                                                                                                                                                                                                                                240 REAAAFRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEI 297
                                                                                                                                                                                                                                                                                                                                                                     LELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVC
                                     10; Gaps
Query Match 41.4%; Score 638; DB 8; Length 309; Best Local Similarity 44.0%; Pred. No. 8.8e-49; Matches 131; Conservative 66; Mismatches 91; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                    244
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Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                         Protein encoded by Prokaryotic essential gene #29955.
         ABU44428 standard; protein; 302 AA
                                                                                                                                                                                                           21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
                                                                                                                                                                                      21-MAR-2002; 2002WO-US009107
                                                    19-JUN-2003 (first entry)
                                                                                                                     Streptococcus mutans
                                                                                                                                          WO200277183-A2.
                                                                                                                                                                03-OCT-2002
ABU44428
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the invention trainers to an interest and under expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense encoding a polypeptide whose expression is inhibited by the antisense continued a polypeptide whose expression is inhibited by the antisense continued in a nucleic acid, (4) an antibody capable of specifically binding the polypeptide, (5) producing the polypeptide; (6) inhibiting callular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway confideration or that has an activity against a biological pathway or the proliferation, or that inhibits callular proliferation; (8) identifying a gene required for callular proliferation of the gene product or that has an activity against a biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound a activity; (11) a culture computed that inhibits the extent or by which each of the strains is present in a culture or collection of a proliferation of an organism. The antise mucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for callular proliferation to a solution of a compound that inhibits the contained for identifying the cardidate molecic acids required for callular proliferation to a solution of a compound that inhibits the caption of a compound that inhibits or serional action of a compound and activity of a compound and activity of a compound activity of a c
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                                                                                                                                                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 CGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELVGLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 MAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTREAA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 NRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKG
                                                                                                                          Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.8%; Score 536; DB 6; Length 30
39.3%; Pred. No. 1.3e-39;
:ive 64; Mismatches 111; Indels
                                                                                                                          Ohlsen KL,
Forsyth RA,
                                                                                                                             ď
                                                                                                                          Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID NO 72352; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                          Malone C,
Carr GJ,
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 39.3<sup>3</sup>
Matches 116, Conservative
                                                                         (ELIT-) ELITRA PHARM INC.
                                                                                                                          Zamudio C,
Trawick JD,
                                                                                                                                                                                                    2003-029926/02
                                                                                                                                                                                                      WPI; 2003-029926,
N-PSDB; ACA48298
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                                                                                                                             Wang Wall
  셤
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Length 306; Indels

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124 NRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKG 183

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ADN27185 standard; protein; 299

RESULT 9 ADN27185

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à 음

CGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELVGLK 123

64

LLELKNVSKTIRGKKI I EGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV

69; Mismatches 106; Score 535.5; DB (Pred. No. 1.5e-39)

34.7%; 38.5%;

Query Match Best Local Similarity 38.54 Matches 115; Conservative

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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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                                                                                                                                                                                                                                                                                                                                                        Recombinant DNA construct; transformed plant; improved plant property;
241 MRKGFELEENQSIVLKDYNKTNIAAAVKVLVANDIDIYQVRMVRKSLEEVFLDMT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1, SEQ ID NO 17122; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen X,
                                                                                                                                         ADS28089 standard; protein; 306 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-2002; 2002US-0360039P.
                                                                                                                                                                                                                                                                                                   Bacterial polypeptide #17122
                                                                                                                                                                                                                                                   (first entry)
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HINKLE G J.
SLATER S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-061375/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003233675-A1.
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                                                                                                                                                                                                                                                   02-DEC-2004
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                                                                                                                                                                                              ADS28089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAOY/)
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promoter that the transfer of a recommentation of promoter is positioned to promoter the promoter is positioned to promoter the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and method of producing a transformed plant having an improved property. The plant is a crop plant comparison in improved property comprises transformed plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plants with the crecombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for improving plants with the improved plant properties, e.g. improved cold, heat or drought tolerance, improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistence to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased resistence to plant disease, better growth rate by modification of content, improved plant growth and development under at least one stress content, improved plant growth and development under at least one stress providing improved plant growth and development under at least one stress conduction. This sequence represents a bacterial polypeptide used in the printed specification but was obtained in electronic forms of the printed specification but was obtained in electronic invention relates to a recombinant DNA construct comprising a format from USPTO at segdata.uspto.gov/sequence.html

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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a
                                                                               Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Goldman BS
                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 9838; 122pp; English.
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                                                                                                                                                                                                                                                                                          20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                                                                    21-FEB-2002; 2002US-0360039P
                                                      Bacterial polypeptide #9838.
                            02-DEC-2004 (first entry)
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HINKLE G J.
SLATER S C.
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                                                                                                                                                                                                       Bacteria.
ADN27185;
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                                                                                                                                                                                                                                                                                                                                                                  (HINK/)
                                                                                                                                                                                                                                                                                                                                                                                                CHEN/
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Sequence 306 AA;

genome of organism particularly chips for analysis, applicable in

Claim 9; SEQ ID NO 1919; 598pp; Japanese.

Method for disrupting targeted gene in thermostable bacterium and with genome studying gene structure and functions

(NISC-) JAPAN SCI & TECHNOLOGY CORP.

Imanaka T, Atomi H; WPI; 2004-257583/24.

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microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the cecombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties.

The recombinant DNA construct is useful for improving plants with improved plant properties, e.g. improved cold, heat or drought colerance, tolerance to herbicides, extreme osmetic conditions, pathogens or peats, increased resistance to plant disease, better growth rate by modification of the content, improved yield by modification of carbohydrate, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of photosynthesis or by production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic formant from USPTO at seqdata.uspto.gov/sequence.thml.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 VGSLIESPSYYGHLSGYENLRIIATL-KGTPEKDIGRVLEIVRLENOKNKKTNQYSLGMK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELVGLKNRINDKVKTYSLGMR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKGMAVIVSSHLLSEMEL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTREAAAFRKVKVDEAEGGIE 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 VSDLDLSVAEGAVYGFLGPNGAGKSTTLKMILGLVKPTAGSITVFGKTWNHRSRMSILKD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 IEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVCGVSVKENFEKA-ARH 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene disruption; gene targeting; marker gene; transformation; homologous recombination; hyperthermostable archaebacterium; KOD1; gene structure; gene function; enzyme activity; medicine; forensic science; food; drug inspection; molecular biology; immunology.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 LSIQKD-----EVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEIT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.5%; Score 516; DB 8; Length 299; 41.0%; Pred. No. 8.3e-38; ive 53; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermococcus kodakaraensis KOD1 protein sequence SeqID1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADN48041 standard; protein; 311 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 299 AA;
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This invention relates to a novel method for targeting disruption of an arbitrary gene in a genome of an organism which comprises providing the whole sequential data of the genome of such organism, selecting at least larbitrary region in the sequence, providing a vector that contains a sequence homologous with the selected region and a marker gene, transformation, and homologous recombination. The genome is preferably the genome of a hyperthermostable archaebacterium, particularly the genome of a hyperthermostable archaebacterium, particularly the genome of a gene in the genome of an organism, which is applicable in studying gene structure and functions as well as enzyme activities of encoded proteins and useful in medicine, forensic science, food or drug inspection, molecular biology and immunology. With this method, the disruption of a gene at an arbitrary position in a genome can be activitied of filtering and reliably. The present sequence is that of a protein encoded by the genome of Thermococcus kodakaraensis which was derived using the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGVSVKENPEKAARHIGAIVENPELYKFLTGYQNLQQYA---RMTKGVTKKKIDEIVELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 EKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQAD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 D-GKTILPSSHILSEVEIISDRIGIISKGKL----LISGSQDEIKRKFIEGRYMIVAET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 8; Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.5%; Score 501; DB 8; Length 311
38.3%; Pred. No. 2e-36;
ive 63; Mismatches 103; Indels
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30-AUG-2002; 2002JP-00319011 29-AUG-2003; 2003WO-IB003597

WO2004022736-A1.

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant comprising the recombinant DNA construct and of producing a transformed plant construct and growing the transforming a plant with the recombinant DNA construct is useful for improving plant, where the polymucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for producing plant with the improved plant properties, e.g. improved cold, heat or drought tolerance, colerance to herbicides, extreme osmocific conditions, pathogens or persent content, improved yield by modification of carbohydrate, increased rate of homologous recombination, modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of protein yield and/or content, improved lignin production of carbohydrate, nitrogen or providing improved lignin production of another at least one stress condition, improved lignin production of improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the printed specification but was obtained in electronic forms from ispendented.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
           Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; peet tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; plant growth regulator; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
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                                                                                                                                                                                                                                                                                                                           20-FEB-2003; 2003US-00369493.
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GOLDMAN B S.
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SLATER S C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 306 AA;
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                                                                                                                                                                                               Bacteria
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GVSVKENPEKAARHIGAIVENPELYKFLTGYQNLQQYA---RMTKGVTKKKIDEIVELVG 121 5 LELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVC 64 48; 32.0%; Score 493; DB 8; Length 306; 36.4%; Pred. No. 1e-35; tive 67; Mismatches 91; Indels Conservative Similarity Best Local Sim Matches 118; 65 Query Match ઠે 셤 ò

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with KGMAVIVSSHLLSEMELMCDRIALIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTRE 241 Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide. 242 AAAFRKVKVDEAEGGIELSIQKDEVPDLIK----------HLTDSGV Goldman BS; Chen X, Claim 1; SEQ ID NO 1297; 122pp; English. 279 RLYEVKAVNKSLEDRFLEITADKE 302 280 TIISLEIBEPSLEDVFLKTIYRRE 303 Ź ADN18644 standard; protein; 308 Cao Y, Hinkle GJ, Slater SC, 20-FEB-2003; 2003US-00369493 21-FEB-2002; 2002US-0360039P Bacterial polypeptide #1297. (first entry) WPI; 2004-061375/06. CAO Y. HINKLE G J. SLATER S C. CHEN X. GOLDMAN B S. US2003233675-A1. 02-DEC-2004 18-DEC-2003. ADN18644; 182 Bacteria. CAOY/) (HINK/) (SLAT/) GOLD/) CHEN/ RESULT 12 ADN18644 ద ò 요 ð 용 셤 ò

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties. LKARINDKVKTYSLGMRORLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTRE 181

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improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic form at from USPTO at segdata.uspto.gov/sequence.html.
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Sequence 308 AA;

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64 GYDIFKEPLKAKERLGFLPENATIYEELTAWRNLDFPASFYRMSKQEKEKRIEELLKLVG 123
                                                                                                                                                                                                                     241
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                                                                                                                                                                                                    LKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTRE 181
                                                                                                                                                                                                                                                                                                   227
                                                                                                                                                                                                                                                                                                                                    AAAFRKVKVDEAEGGIELSIQKDEVPDLIK---------HLTDSGV 278
                                                                                                                                                                                                                                                                                                                                                               LEGY-EIKIETKOPLPEL----EIPDIIRIEKTTENKAIIPAKSDIRESISEELAKKGI 281
                                                                                   5 LELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVC
                                                                                                                                 GVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYA---RMTKGVTKKKIDEIVELVG
                                                                                                                                                                                                                                                                   KGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTRE
                                   Gaps
                                   48;
32.0%; Score 493; DB 8; Length 308; 36.4%; Pred. No. 1e-35; tive 67; Mismatches 91; Indel8
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TIISLEIEEPSLEDVFLKTIYRRE 305
                                   Conservative
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                 Best Local Simi
Matches 118;
 Query Match
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ADN18683 standard; protein; 318
                  Bacterial polypeptide #1336.
            (first entry)
            02-DEC-2004
      ADN18683;
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Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; plant tolerance; heat tolerance; pathogen teconomiation; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

20-FEB-2003; 2003US-00369493 US2003233675-A1

Bacteria

21-FEB-2002; 2002US-0360039P.

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The invention relates to a recombinant DNA construct comprising a provide for expression of a polynuclectide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a cransformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property. The plant is a crop plant comprising an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for improving plant properties. CC colerance to herbicides, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition. Improved plant growth and development under at least one stress condition. Improved plant growth and development under at least one stress condition. Improved plant growth and development under at least one stress condition. Improved plant growth and approved galactomannan production. Note: The sequence data for this patent did not form at recombine the printed specification but was obtained in electronic
                                                                                                                                                                                                                                 New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VIEVRNLRK-LYPKKIPLPFRKVEWFEALKGITFRVKKGELFGLLGPNGAGKTTTIKILT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 GHMSITAGEIAVCGVSVKENFEKAARHIGAIVENPE-LYKFLTGYQNLQQYAR---MTKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 TLLEPSSGEAKVLGLDVVKDAREIRKRINLVARGERTLYWRLTAYENLRYFASIYYIPRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 VTKKKIDEIVELVGLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPINGLDPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 AVFVRELVRIVDEEGKTVLLTTHYMNEAEELCDRIAIIDHGKIIALNTPEGLKR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---MVRNDTIVEVRVRNYPGVNPFGLVKVDDRNGVVILRGSLEEBEIPKLVEFLVKSNAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 LLELKNVSKTIRGKKI------IEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 IREIRDYLRKLTREKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 format from USPTO at segdata.uspto.gov/sequence.html
                                                                                                                                        Goldman BS
                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1336; 122pp; English.
                                                                                                                                        Chen X,
                                                                                                                                        Hinkle GJ, Slater SC,
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Matches 112; Conservative
              HINKLE G J.
SLATER S C.
CHEN X.
                                                                                           GOLDMAN B S.
                                                                                                                                                                                    WPI; 2004-061375/06.
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(SLAT/)
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227 181

RESULT 14

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a crop plant cannot as maize or soybean. The method of producing a transformed plant cannot an improved property. The plant is a crop plant cannot an improved property comprises transforming a plant with the calmant DNA construct and growing the transformed plant, where the recombinant DNA construct is useful for improved plant properties. The recombinant DNA construct is useful for producing plants with the recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, colerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                     184 MAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTREAA 243
                                                                                                                                      242 PIPELRHEEITRVERLAPNRIILFARSDIREWLSQYLTSKGVTILSLEVEEPSLEDVFMK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                            --- AEGGIELSIQKDEVPDLIKHLIDSGVRLYEVKAVNKSLEDRFLE
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                                                                                                                                                                                                                                                                                                                                                                                                                        ADS27537 standard; protein; 221 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacterial polypeptide #16570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-2003; 2003US-00369493
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                                                                                                               244 AFRKVKVDE----
                                                                                                                                                                                                                                                                               302 TIYGRDE 308
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GOLDMAN B S.
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SLATER S C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADS27537;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HINK/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 SVKENFEKAARHIGAIVENPELYKFLIGYQNLQQYA---RMTKGVTKKKIDBIVELVGLK 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Method for disrupting targeted gene in genome of organism particularly thermostable bacterium and with genome chips for analysis, applicable in
                                                                                                                                                                                                                         gene disruption; gene targeting; marker gene; transformation; homologous recombination; hyperthermostable archaebacterium; KOD1; gene structure; gene function; enzyme activity; medicine; forensic science; food; drug inspection; molecular biology; immunology.
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ilarity 36.8%; Pred. No. 1.9e-35;
Conservative 70; Mismatches 108; Indels 16; Gaps
                                                                                                                                                                           Thermococcus kodakaraensis KOD1 protein sequence SeqID408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; SEQ ID NO 408; 598pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        studying gene structure and functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NISC-) JAPAN SCI & TECHNOLOGY CORP.
        ADN46530 standard; protein; 309 AA.
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                                                                                                                     (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-257583/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004022736-A1.
                                                                                                                     01-JUL-2004
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homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
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Sequence 221 AA;

2; 61 JAVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKK-IDEIVEL 119 | : | : : | : | | | | | | | : | | : | | | | | | | : | | | | | | : | | | | | : | | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 1 LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGE 60 2; Gaps Query Match 31.5%; Score 485; DB 8; Length 221; Best Local Similarity 46.2%; Pred. No. 3.4e-35; Matches 98; Conservative 51; Mismatches 61; Indels 180 REKGMAVIVSSHLLSEMELMCDRIALIONGKL 211 윱 ò ઠે 셤 ઠે 유 ò

completed: July 13, 2006, 13:43:55 ne : 197 secs Search co AGE BLANK (USPTO)

GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

July 13, 2006, 13:44:12; Search time 40 Seconds (without alignments) 738.464 Million cell updates/sec Run on:

Title: Perfect score:

US-10-510-941-2 1542 1 LETLLELKNVSKTIRGKKII.......KSLEDRFLEITADKEEAQHV 307

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_80:# 1: pir1:# 2: pir2:# 3: pir3:# 4: pir4:#

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ABC transporter (A ABC transporter (A Similar Dec transporter, A ABC transporter, A ABC transporter, A ABC transporter (A ABC transporter (A ABC transporter, A transporter, A transporter, A transporter, A ABC-type MDR transporter (A ABC-type MDR transporter, A ABC-type multidrug daunorubicin resis Description SUMMARIES D69822 AD1169 AF1526 G96916 E69771 H96917 AD1642 D97272 D97272 E883705 B83705 D97151 T09008 H71008 H Query Match Length DB 463.5 463.5 461.5 451.5 444.5 Result No.

transposase (08) /	ABC transporter AT	ABC transporter AT	ABC transporter, A	ATP-binding protei	spaF protein - Bac	ABC transporter (A	ABC transport prot	ABC transporter (A	gliding motility p	ABC transporter (A	hypothetical prote	ABC transporter (A	probable ABC-type	ABC transporter (A	probable ATP-bindi
P83781	F96932	AE2102	F87655	AE2008	140516	C69012	T43103	E96920	T44443	B83912	D72257	E84136	T36316	B83686	G71131
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28.7	28.	28	27	7	'n	~	••								
	431.5 28.	431.5 28	430.5 27	428 27	425 2,	424.5 2	424	422.5	421.5	421.5	421	420.5	420.5	420	420

ALIGNMENTS

RESULT 1
Decoration (ATP-binding protein) homolog yhcH - Bacillus subtilis C.Speries: Bacillus subtilis
 C.Decries: Decriped Sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
C;ACCESSION: D03022 R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte C : Bron S : Bronillar S : Bruchi C V : Caldwell B : Cannan V : Carter N M : Ch
A.; Bhrlid, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nacute 390, 249-250, 159, A.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallo
<pre>lecn, J.; Harwood, C.K.; Hendut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.: Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinoiz</pre>
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauecly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekionchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama T. Winters D. Winat A. Yamamofo H. Yamane K. Yasumoto K. Yara K. Yoshida
A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis A:Reference number: A69580: MIID:98044013: PMID:9184377
A, Accession: D69822
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A; wciecule crype:
A, Cross-references: UNIPROT: P54592; UNIPARC: UP10000060122; GB: Z99108; GB: AL009126; NID
A/Experimental source: strain 168
Cycaractes: A;Gene: yhcH
C;Keywords: ATP; nucleotide binding; P-loop R:20-209/Domain: ATP-hinding cassette homology cARCs
F;37-44/Region: nucleotide-binding motif A (P-loop)
Ouery Match 66.6%; Score 1027; DB 2; Length 305; Best Local Similarity 65.1%; Pred. No. 1.3e-57; Matches 200; Conservative 47; Mismatches 56; Indels 4; Gaps 2;
QY 1 LETLIELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGE 60
Db 1 MKTVLELKNVTKNIRGRTIIDDLSFTIREGEVFGFLGPNGAGKTTTIRMWGLMKLSKGD 60
Qy 61 IAVCGVSVKENFEKAARHIGAIVENPELYKPLIGYQNLQQYARMIKGVIKKKIDEIVELV 120
 Db 61 VLICGQSITKEYAKAIKHIGAIVENPELYKFLSGYKNLQQFARMVKGVTKEKIDEVVELV 120
QY 121 GLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLKKLTR 180
Db 121 GLTDRIHDKVKTYSLGMRQRLGLAQCLLHDPKVLILDEPTNGLDPAGIREIRDHLKKLTR 180

181 EKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTR 240

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G97260 G97006 H75157 B97006

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62

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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-301 <GLA>
A;Cross-references: UNIPROT:Q92DR3; UNIPARC:UPI0000CC33A; GB:AL592022; PIDN:CAC95982.1
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin0750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Age transporter, ATP-binding component CAC0138 [imported] - Clostridium acetobutylicum C;Species: L4-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004
C;Accession: G9516
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Leel, Balty, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium ClA;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: G96916
A;Accession: G96916
A;Accession: G96916
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A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTRE 241
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46.0%; Pred. No. 9e-36;
:ive 60; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                     89; Indels
                                                                                                                                                                                                                                                    Query Match
47.3%; Score 730; DB 2;
Best Local Similarity 49.5%; Pred. No. 6.2e-39;
Matches 147; Conservative 57; Mismatches 89;
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Matches 139; Conservative
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C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
C; Accession: AD1169
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karet, U.
Science 24, 849-852, 2001
A; Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simces, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Reference number: AB1077; MUID:21537279; PMID:11679669
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A; Residues: 1-301 <GLA>
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A; Experimental source: strain EGD-e
C; Genetics:
A; Genetics:
A; Genetics:
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A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                 transporter (ATP-binding protein) lmo0756 [imported] - Listeria monocytogenes (strai
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                           ERGMAVIVSSHLLSEMELMCDRIAILQKGKLIDIQNVKDENIDENDTYFFQVEQP---SE
                                                                              EAAAFRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEITAD
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Best Local Similarity 49.89
Matches 149; Conservative
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ABC transporter, ATP-binding protein CAC0147 [imported] - Clostridium acetobutylicum C;Species Clostridium acetobutylicum C;Accession: H96917
R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Le; Daly, M.J; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J; Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C]
A;Reference number: A96900; MUD:21359325; PMID:21359325
A;Accession: H96917
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-318 <KUR>
A;Coss-references: UNIPROT:Q97MP5; UNIPARC:UPI00000C9D8B; GB:AE001437; PIDN:AAK78131.1
A;Gene: CAC0147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gispecies: Listeria innocus
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
Cipacesion: Ab1642
Richaer, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.D.; Jonensus-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.S.; Jonenson, E.; Mathors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; I.A.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland A; Title: Comparative genomics of Listeria species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q92B73; UNIPARC:UPI0000CC61A; GB:AL592022; PIDN:CAC96908.1
A;Experimental source: strain Clip11262
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABC transporter (ATP-binding protein) homolog lin1677 [imported] - Listeria innocua (st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B----AAAPRKVK------VDEAEG--GIELSIQKDEVPDLIKHLTDSGVRLYEVKAVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
43.3%; Score 667; DB 2; Length 318
Best Local Similarity 42.9%; Pred. No. 6.1e-35;
Matches 133; Conservative 69; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 KSLEDRFLEI 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::||||::|:
QNLEDRYIEL 307
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A,Status: preliminary
A,Molecule type: DNA
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                                                                                                                                                                                                                                                                                 Age transporter (ATP-binding protein) homolog ydbJ - Bacillus subtilis
C;Species: Bacillus subtilis
R;Kunst, F:; Ogasawara, N:; Moszer, I:; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Baron, S; Brudeli, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ebrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A;Bullors: Poulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A; Harwood, C.R.; Harmaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Socffone, F.; Sekiguchi, J.; Sekowska, A.; Serok
A;Authors: Yoshikawa, H.F.; Zumetein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Voshida, R
A;Authors: Yoshikawa, H.F.; Zumetein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044013; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-308 «KUN»
A; Cross-references: UNIPROT: P96605; UNIPARC: UPI00005FF63; GB: 299106; GB: AL009126; NID: q
C; Genetics:
                               244 SKLPFVYEVKNNBDKISAAIQYGTSPKVIABLMKNSVEVIEFYKEHKTLEDRFMQIVEGE 303
243 AAFRKV-KVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEITADK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTRE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 AVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELVG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAFRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLE-ITAD 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ETLLELKONVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary; nucleic acid sequence not shown; translation not shown
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42.7%; Pred. No. 3.1e-35;
iive 71; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: ATP; nucleotide binding; P-loop F;21-210/Domain: ATP-binding cassette homology <ABC>F;38-45/Region: nucleotide-binding motif A (P-loop)
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A;Molecule type: DNA
                                                                                                        EE 303
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Query Match

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protein from GDSL (phospholipase B) family of lipolitic enzymes [imported] - Clostridium () Species: Clostridium acetobutylicum () Species: Clostridium acetobutylicum () Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004 () Accession: D9722. R) Accession: D9722. R) D972, B. Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R. A. Bennett, G.N.; Koonin, B.V.; Smith, D.R. A. A. Bennett, G.N.; Koonin, B.V.; Smith, D.R. A. Fitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Classic Energy of the Colorest Producing Producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-300 «KUR»
A;Cross-references: UNIPROT:Q97ETO; UNIPARC:UPI00000D7564; GB:AE001437; PIDN:AAK80967.1
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABC transporter (ATP-binding protein) BH0445 [imported] - Bacillus halodurans (strain C C, Species: Bacillus halodurans C; Species: Bacillus halodurans (c, Species: O1-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004 C; Accession: B83705 C; Accession: B83705 C; Accession: K; Takat, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir Nucleic Acids Res. 28, 4317-4331, 2000 A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83550; MUID:20512582; PMID:11058132 A; Accession: B83705 A; Accession: B83705 A; Accession: B83705 A; Accession: B83705 A; Accession: Carbot C, C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 CGYSILHNYVKAMESVGCIVEGPDLYEXMSGEDNLEMLAAMDKNVTNEDIEYAVNLVNME 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 NRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 KSIKDKISTYSLGMKQRMGIAQALMKRPKLLILDEPTNGLDPAGINDLRNLIQRLSKEEK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 MAVIVSSHILLSEMELMCDRIALIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTREAA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 AFRKVKVDEAEGG--IELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEITADK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 K-NSWRIDSRINGSKLEASVDEEKLISINDSFLSNGIKIKFASSKQRNLEDLFLNITEDK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.4%; Score 638; DB 2;
40.7%; Pred. No. 3.8e-33;
tive 85; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 40.7%
Matches 122; Conservative
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Query Match

Best Local Similarity 38.54

Matches 115; Conservative
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A; Reference number: AB1077; MUID:21537279; PMID:11679669 A; Residues: Dilannary A; Molicule type: DNA A; Residues: 1-306 <GLA> A; Molicule type: DNA A; Residues: 1-306 <GLA> A; Residues: 1-306 <G
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45.3%; Pred. No. 3.4e-33;
tive 57; Mismatches 104; Indels
                                            Indels
Best Local Similarity 45.0%; Pred. No. 2.5e-33; Matches 134; Conservative 59; Mismatches 103;
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Best Local Similarity 45.3%
Matches 135; Conservative
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Dacitracin transport protein bcrA - Bacillus licheniformis
C;Species: Bacillus licheniformis
C;Species: Bacillus licheniformis
C;Species: Bacillus licheniformis
C;Species: A-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 05-Oct-2004
C;Accession: 577627
R;Podlesek, Z.; Comino, A.; Herzog-Velikonja, B.; Zgur-Bertok, D.; Komel, R.; Grabnar, Mol. Microbiol. 16, 969-976, 1995
My-Title: Bacillus licheniformis bacitracin-resistance ABC transporter: relationship to A;Reference number: 877627, MUID:96059642; PMID:7476193
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-306 <POD>
A;Residues: 1-306 <POD>
A;Cross-references: UNIPROT:P42312; UNIPARC:UPI0000126845; EMBL:L20573; NID:g466477; PI
A;Experimental source: strain ATCC 9945A
                                                                                                                                                                                                                                                                                         61 VELFG--EKNPTRSIYKKIGSIIEYPGFYPNLTAEENLDIHRRWMKIENOKRINETLTWV 118
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                                                                                                                                                                                             1 MKYLVRTFNLTKKYKNTSVVENLNLNINIEOGQIYGFLGKNGAGKTTTLMILGLMKISTGE
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179 CKDRGITILVSSHLLSEIBQLATKIGIIDKGHLIEELTYDDLQKRNKKYLKLKVSD----
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                                                                                                                                                                  1 LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGE
                                                                                                                                                                                                                                                              61 IAVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 TREKGMAVIVSSHLLSEMELMCDRIALIONGKLRDIOHVHGPARDEKKRYYIQADDTQAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Keywords: antibiotic resistance; ATP binding; nucleotide binding; P-loop F;20-209/Domain: ATP-binding cassette homology <ABC>F;37-44/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGE
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                                                                           Length 306;
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                                                                      ; Score 523; DB 2; Length 30; Pred. No. 6.6e-26; 65; Mismatches 106; Indels
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                                                                        33.9%;
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 113; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 RFLEIT 298
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                                                                                              Similarity
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                                                                                              Best Local Sim
Matches 121;
    C;Genetics:
A;Gene: CAC2040
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                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                              ABC transporter, ATP-binding protein CAC0288 [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 31-Dec-2004 C;Accession: B96935 C;Accession: B96935 C;Accession: B69035 C;Accession: B69035 C; Daly, M.J.; Bentet, G.; Cmelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol: 183, 4823-4838, 2001 A;Aitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325
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R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325, PMID:21359325
A;Accession: D97151
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-306 <KUR>
A;Residues: UNIPROT:Q97HH1; UNIPARC:UPI00000CA3C9; GB:AE001437; PIDN:AAK79999.1; A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:097MBO; UNIPARC:UPI00000C9DFE; GB:AE001437; PIDN:AAK78269.1;
C;Genetics:
A;Gene: CAC0288
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                                                                                                                                                                  FGKDLKQHRLDILKNIGALVESPSYYPHLSGEDNLETVRKIVK-VPKSRIAEVLELVRLT 125
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                                           MAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTREAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 AF---RKVKVDEAEGGIELSIQKD-EVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEIT
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; Pred. No. 2.3e-26;
49; Mismatches 57;
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Best Local Similarity 48.68
Matches 101; Conservative
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67
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A;Molecule t;
A;Residues: 1
A;Cross-refer
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A;Cross-references: UNIPROT:031054; UNIPARC:UPI00000B5C5D; EMBL:AF026542; NID:g2502065;
A;Experimental source: strain FF22
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 05-Oct-2004
C;Accession: T09008
R;Hynes, W.L.; Ferretti, J.J.; Tagg, J.R.
Appl. Environ. Microbiol. 59, 1969-1971, 1993
A;Title: Cloning of the gene encoding streptococcin A-FF22, a novel lantibiotic A;Reference number: A58598; WUID:93319301; PMID:8328813
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----TDSGVRLYEVKAVNK 288
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
   239 TREAAAFRKVKVDEAEGGIELSIQKDEVPDLIKHL-
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SLEDYFVKL 299
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                                                                                                                                       25;
                                                                                              Length 299;
                                                                                                                                         Indels
                                                                                                32.7%; Score 504.5; DB 2; 39.4%; Pred. No. 9.4e-25; iive 59; Mismatches 102;
C,Genetics:
A,Gene: scarcescretic biosynthesis
C,Keywords: antibiotic biosynthesis
P,20-209/Domain: ATP-binding cassette homology <ABC>
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Job time : 41 secs
                                                                                                                                             Matches 121; Conservative
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289 ENLEDIF 295
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Query Match
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P54592 bacillus su
Q6i117 bacillus an
Q6i110 bacillus th
Q6i110 bacillus th
Q73be3 bacillus ce
Q3em11 bacillus th
Q8151 bacillus th
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Q8142 bacillus th
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Q8142 bacillus ce
Q6han5 bacillus ce
Q6han7 bacillus ce
Q8140 listeria mo
Q64c1 listeria mo
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                                                                                                       1 LETLLELKNVSKTIRGKKII.......KSLEDRFLEITADKEEAQHV 307
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Q81tb0 )
Q97mq4
Q41ax1
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                   2849598 segs, 925015592 residues
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YHCH BACSU
Q8EQIS OCEIH
Q61117 BACAN
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Q97MQ4_CLOAB
Q41AX1_9BACI
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Listing first 45 summaries
                                  OM protein - protein search, using sw model
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Q630K0
Q8Y8Y6
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                                                                                                                                                                                                                                                            1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                      US-10-510-941-2
1542
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Match Length DB
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                                                                                                                         BLOSUM62
                                                                                                                         Scoring table:
                                                                                               Perfect score:
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مثن ا	307 AA.	PRT;	RY;	PRELIMINARY;		T 1 7 BACLD 065M37 BACLD	RESULT 1 Q65M37 BACLD ID Q65M37 AC Q65M37
	ALIGNMENTS	ALIG					
Q71z32 listeria mo	LISME	Q71Z32_LISMF	N	306	41.4	638	45
	LISMO	Q4EEG7_LISMO	10	306	41.4	638	4.
Q65dd4 bacillus li	BACLD	O65DD4 BACED	N (000	41.4	859	4. 4.
Q8y6p8 listeria mo	LISMO	Q8Y6P8_LISMO	0	306	41.4	639	41
	LISMO	04 EMV3	~	306	41.4	639	40
Q92b73 listeria in	LISIN	Q92B73	7	306	41.6	641	39
	CLOTE	Q895C2	0	303	42.7	658.5	38
	BACCR	081CN4	1 (1	319	42.8	660.5	37
Oswilz bacilius ci	BACER	OSWIIZ BACSK	7 C	30.7	43.2	666.3 663	3,5
	CLOAB	Q97MP5_CLOAB	~	318	43.3	667	34
Q2w176 clostridium	CLOBE	Q2WL76 CLOBE	~	304	43.5	670	33
P96605 bacillus su	BACSU	P96605 BACSU	7	308	43.5	671.5	

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
PubMed=15383718; DOI=10.1159/000079829;
Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,
Ehrenreich A., Gottschalk G.; Henne A. Liesegang H., Merkl R.,
The complete genome sequence of Bacillus licheniformis DSM13, an
organiam-with-great industrial-potential.";
J. Mol. Microbiol. Biotechnol. 7:204-211(2004). 25-OCT-2004, integrated into UniProtKB/TrEMBL.
25-OCT-2004, integrated into UniProtKB/TrEMBL.
25-OCT-2004, entry version 1.
07-FEB-2006, entry version 15.
07-FEB-2006, entry version 15.
NAME-YICH, OrderedLocusNames=BL03183, BL100969;
Bacillus licheniformis (strain DSM 13 / ATCC 14580).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

PULDEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
PubMed=15461803; DOI=10.1186/gb-2004-5-10-r77;
Rey M.W., Ramaiya P., Nelson B.A., Brodov-Karpin S.D., Zaretsky E.J., Tang M.W., Lopez de Leon A., Xiang H., Gusti V., Clausen I.G., Olsen P.B., Rasmussen M.D., Andersen J.T., Joergensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D., Berka R.M.;
"Complete genome sequence of the industrial bacterium Bacillus Inchniformis and comparisons with closely related Bacillus species."; Genome Biol. 5:RESEARCH077.12(2004).
-1- SIMILARITY: Belongs to the ABC transporter family.

Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License EMBL; AE017333; AA039877.1; -; Genomic_DNA.
R GO; GO:0005224; R:ATP binding; IEA.
R GO; GO:000166; F:ATP binding; IEA.
R GO; GO:000166; F:ATP binding; IEA.
R GO; GO:000166; F:ATP binding; IEA.
R GO; GO:0006810; P:ATRANSPORT; IEA.
R GO; GO:0006810; P:Transport; IEA.
R GO; GO:0006810; P:Transport; IEA.
R InterPro; IPR003533; AAA, ATPase.
R InterPro; IPR003533; AAA, ATPase.
R Pfem; PF000005; ABC_transporter; 1.
R PROSITE; PS00211; ABC_TRANSPORTER 1; UNKNOWN_1.
R PROSITE; PS00211; ABC_TRANSPORTER 2; 1.
R PROSITE; PS00213; ABC_TRANSPORTER 2; 1.
R ATP-binding; Complete proteome; Nucleotide-binding; Transport.
SEQUENCE 307 AA; 34448 MW; A7ABDB7C38EBFABA CRC64;

Length 307; 99.9%; Score 1540; DB 2;

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EMBL; X96983; CAA65691.1; -; Genomic_
EMBL; Z99108; CAB12736.1; -; Genomic_
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Matches 200; Conservative
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SEQUENCE
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                                                                                                         IAVCGVSVKENPEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELV
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"A 22 kb DNA sequence in the cspB-glpPFKD region at 75 degrees on
Bacillus subtilis chromosome.";
Microbiology 142:3021-3026(1996).
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                          Indels
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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Hypothetical ABC transporter ATP-binding protein yhcH.
Name=yhcH; OrderedLocusNames=BSU09080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
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01-OCT-1996, sequence version 1.
07-MAR-2006, entry version 41.
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=168;
                          Mismatches
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     Pred.
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MEDLINE=97124185; PubMed=8969498;
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  99.78;
                             Conservative
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     Similarity
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Best Local Sim:
Matches 306;
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Distributed under the Creative Commons Attribution-NoDerivs License
Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A., Tosaco V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzensger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumatein E., Yoshikawa H., Danchin A.; Pengarana A., Samanoto M., Baccin B., Senilus A., Shintii A., Sh
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GenomeReviews; AL009126 GR; BSU09080.

Subtilist; BG1136, yhcH.

BioCyc; BSUB143:BSU0908-MONOMER; -.

BioCyc; BSUB143:BSU0908-MONOMER; -.

InterPro; IPR003593; AAA_ATPRAGe.

InterPro; IPR003593; AAA_ATPRAGe.

InterPro; IPR003593; ABC_transp_like.

ProDom; PD000006; ABC_transp_like.

ProDom; PD000006; ABC_transporter; 1.

PROSITE; PS50893; ABC_TRANSPORTER 1; 1.

PROSITE; PS50893; ABC_TRANSPORTER 2; 1.

ATP-binding; Complete proceome; Hypothetical protein;

Nucleotide-binding; Transport.

CHAIN 1305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:249-256(1997).
--- SIMILARITY: Belongs to the ABC transporter family.
--- SIMILARITY: Contains 1 ABC transporter domain.
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/FTId=PRO_000093143.
ABC transporter.
ATP (Potential).
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QBEQIS OCEIH
1D QBEQIS_OCEIH PRELIMINARY; PRT; 307 AA.
AC QBEQIS;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
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Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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QEHLJO;
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Matches 160; Conservative
                               Bacillus cereus group.
                                                                                                                                                     STRAIN=Sterne;
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                                                                                                                                                                                                                                                       STRAIN=HTEB31 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments.";
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                                                                                                                  Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
NCBI_TaxID=182710;
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PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Complete proteome; Nucleotide-binding; Txx
SEQUENCE 307 AA; 34261 WW; CDFBBF002C9C2F5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.3%; Score 806; DB 2; 51.3%; Pred. No. 1.7e-37; ive 71; Mismatches 72,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATPase activity; IEA.
GO; GO:000166; F:ATPase activity; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
R GO; GO:0000160; P:ransport; IEA.
R InterPro; IPR00359; AAA ATPase.
R InterPro; IPR00359; ABC_transp_like.
R Pfam; PF00005; ABC tran; 1.
R Pfam; PF000005, ABC_transporter; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM03382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BA000028; BAC13670.1; -; Genomic_DNA.
BioCyc; OIHE182710:OB1714-MONOMER; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 30:3927-3935(2002)
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OrderedLocusNames=BAS1274;
                      21-FEB-2006, entry version 27.
ABC transporter ATP-binding protein.
OrderedLocusNames=OB1714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2006, entry version 12.
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Matches 153; Conservative
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Match

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061117 1D 06 AC 06 DT 19 DT 19 GN 07 OS Ba

CGHSIRTEREKALEQIGAIVENPELYDYMTGMQNLKHPANMAITPISKERIAEIVKLVEL 124 KNRINDKVKTYSLGMRORLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREK 182 183 GMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPAR-DEKKRYYIQADDTQALTRE 241 S VVKLENVRKKIGGTEIIRGLSFEVREGEVYGFLGPNGSGKTTTIRAMTGLISMTEGDITI 64 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License 242 AAAFRKVKVDBAEGG-IELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEIT 298 185 NIAVIVSSHLLSEIELMCDRVVIIKQGEFVQEYNLHEQAKHDETVVVAFEVDQVQKA---Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin B., Tice H.;
"Complete genome sequence of Bacillus anthracis Sterne.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: Belongs to the ABC transporter family. 4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV CGVSVKENPEKAARHIGAIVENPELYKPLTGYQNLQQYARMT-KGVTKKKIDEIVELVGL 19-JUL-2004, integrated into UniProtKB/TrEMBL.
19-JUL-2004, sequence version 1.
19-JUL-2004, sequence version 1.
19-JUL-2004, sequence version 1.
10-Treas-2006, entry version 14.
ABC transporter, ATP-binding protein; possible multidrug transporter.
Name=bcrA; OrderedLocusNames=BT9727 1246;
Bacillus thuringiensis subsp. konkukian.
Bacteria; Firmicutes; Bacillales; Bacillus;
Bacillus cereus group.
NCBI_TAXID=180856; Gaps 10; Length 300; 69; Indels PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Nucleotide-binding; Transport.
SEQUENCE 300 AA; 33378 WW; 4FBIA80D119ACD92 CRC64; 51.2%; Score 789; DB 2; 53.7%; Pred. No. 1.5e-36; ive 59; Mismatches 69; NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]. EMBL; AE017225; AAT53594.1; -; Genomic_DNA.GO; GO:0005524; F:ATP binding; IEA.GO; GO:0016887; F:ATPase activity; IEA.GO; GO:0000166; F:nucleotic binding; IEA.GO; GO:0006810; P:ransport; IEA.InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003593; AAA_ATPase.
Fam; PF00005; ABC_transp_like.
Probom; PD00005; ABC_transp_like.
Probom; PD00005; ABC_transp_like.
SMART; SM00382; AAA; I. NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] 300 AA

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which is

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64 CGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMT-KGVTKKKIDEIVELVGL 122
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                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 -KANEIIKGKAQRNVIVVSVTKEEIPQLVKKLVNEDVLVYGVTVQNKTLEBEFLAIT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 AAAFRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEIT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

PubMed=14960714; DOI=10.1093/nar/gkh258;

Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,

Shores K.A., Fouts D.E., Tourasse N.J., Angluoli S.V., Kolonay J.F.,

Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;

"The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
adaptations and a large plasmid related to Bacillus anthracis pXO1.";

Nucleic Acids Res. 32:977-988(2004).

- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 VVKLENVRKKIGGTEIIRGLSFEVREGEVYGFLGPNGSGKTTTIRMMTGLISMTEGDITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus cereus (strain ATCC 10987).
Bacteria, Firmicutes, Bacillales, Bacillus, Bacillus cereus group.
NCBI_TaxID=2225523;
Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDB whole genome shotgun (WGS) entry w preliminary data.
-!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Wuclectide-binding; Transport.
SEQUENCE 300 AA; 33506 MW; E0BIID19DB91DC53 CRC64;
                                                                                                                                                           ; DB 2;
2.5e-36;
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%; Pred. No. 2.5e-
55; Mismatches
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07-FEB-2006, entry version 12.
ABC transporter, ATP-binding protein.
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53.9%;
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Best Local Similarity 53.9%
Matches 160; Conservative
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"Identification of anthrax toxin genes in a Bacillus cereus associated with an illness resembling inhalation anthrax.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV
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     Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka I Richardson P., Rubin B., Tice H., "Complete genome sequence of Bacillus thuringiensis 97-27."; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                      Transport
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 300;
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Bacillus cereus group.
NCBI_TaxID=269801;
                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Complete December 2 Nucleocide-binding; Trs SEQUENCE 300 AA; 33378 MW; 4FBLA80D719ACD92 CRC64;

    -I- SIMILARITY: Belongs to the ABC transporter family.

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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 51.2%; Score 789; DB 2; Best Local Similarity 53.7%; Pred. No. 1.5e-36; Matches 160; Conservative 59; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q4MS13;
02-AUG-2005, integrated into UniProtKB/TrEMBL.
02-AUG-2005, sequence version 1.
02-RB-2006, entry version 7.
Bacitracin transport ATP-binding protein borA.
ORFNames=BCE G9241 1372;
Bacillus cereus G9241 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-G9241;
PubMed-15155910; DOI-10.1073/pnas.0402414101;
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Length 300;

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Q63E15_BACCZ
Q63E15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                   ATP-binding, Complete_proteome; Nucleotide-binding; Transport. SEQUENCE 300 Aa; 33353 MW; 5941DAE7B7BDD7A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                       69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORFNames=RBTH 02680;
Bacillus thuringiensis serovar israelensis ATCC 35646.
Bacillus trimicutes; Bacillales; Bacilluscese; Bacillus;
Bacillus cereus group.
NCBI_TaxID=339854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary data.
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53.4%; Pred. No. 2.5e-36;
ive 60; Mismatches 69.
                                                                                                                                                                                                                                                                           PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
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                                                            EMBL; AE017194; AAS40404.1; -; Genomic_DNA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0010869; F:ATP binding; IEA.
GO; GO:0010166; F:nucleotide binding; IEA.
InterPro; IPR003593; AAA_ATPase.
Fam; PF00005; ABC_transp_like.
PF0000; PD00005; ABC_transp_like.
ProDom; PD000006; ABC_transp_like.
FAMAT; SM00382; AAA; I.
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Best Local Similarity 53.4*
Matches 159; Conservative
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Q3EML1_BACTI
Q3EML1;
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ABC transporter, ATP-binding protein; possible multidrug transporter.
Name-bork; OrderedLocusNames=BCB33L1248;
Bacillus cereus (strain ZK / B33L).
Bacieria; Pirmicutes; Bacillales; Bacillaceae; Bacillus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin B., Tice H.; "Complete genome sequence of Ballulus cereus ZK."; Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.8%; Score 78%; DB 2; Length 300;
53.4%; Pred. No. 2.9e-36;
iive 58; Mismatches 71; Indels
                                                                                                                                                                                                                                                                         SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Nucleotide-binding; Transport.
SEQUENCE 300 AA; 33369 MW; 841D6E496F197457 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-0CT-2004, integrated into UniProtKB/TrEMBL. 25-0CT-2004, sequence version 1. 07-FEB-2006, entry version 13.
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                   GO; GO: 0005524; F: ATP binding; IEA.
GO; GO: 0016887; F: ATPase activity; IEA.
GO; GO: 000166; F: mucleculed binding; IEA.
GO; GO: 0000810; P: transport; IEA.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003493; ABC transpolter; IEA.
Probom; PD000005; ABC transpolter; I.
Probom; PD0000006; ABC transpolter; I.
SWART; SM00382; AAA; I.
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EMBL; AAJM01000404; EAO52546.1; -; Genomic_
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016887; F:ATPase activity; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
GO; GO:0006810; P:ransport; IEA.
InterPro; IPR003533; AAA ATPase.
InterPro; IPR003439; ABC_transp_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    llarity 53.4%;
Conservative 5
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NCBI_TaxID=288681;
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QEHANS_BACHK
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SEQUENCE 30
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                                                                                                                                                                                                                                                                                           4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV
                                                                                                                                                                                                                                                                                                                       S SYVKLENVRKKIGGTEIIRGLSFEVREGEVYGFLGPNGSGKTTTIRMYTGLISMTEGDITI
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MEDLINE-22608415; PubMed=12721630; DOI=10.1038/nature01582;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Gacchkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbeek R., Kyrpides N.C.;
"Genome sequence of Bacillus cereus and comparative analysis with
                                                                                                                                                                                                                                                8
                                                                                                                         Transport
                                                                                                                                                                                           Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003, integrated into UniProtKB/TrEMBL.
01-JUN-2003, sequence version 1.
07-FEB-2006, entry version 16.
Bacitracin transport ATP-binding protein bcrA.
OrderedLocusNames=BC1359; ORFNames=BC 1359;
Bacillus cereus (strain ATC 14579 / DSM 31).
Bacillus cereus group.
                                                                                                                                                                                                                                             75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 423:87-91(2003).
-!- SIMILARITY: Belongs to the ABC transporter family.
Pfam; PF00005; ABC_tran; 1.

Probon; PD000006; ABC_transporter; 1.

SWART; SM00382; AAA; 1.

PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.

PROSITE; PS00231 ABC_TRANSPORTER_1; UNKNOWN_1.

ATP-binding; Complete_Croceome; Nucleotide-binding; Trassporter 2; 300 AA; 33561 WW; 14F4E9A8CA306D53 CRC64;
                                                                                                                                                                                             Query Match 50.8%; Score 783; DB 2;
Best Local Similarity 53.9%; Pred. No. 3.3e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AE016877; AAP08341.1; -; Genomic_DNA.
BioCyc; BCER226900:BC1359-WOWGRER. -
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016887; F:ATPase activity; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003493; AAA_ATPase.
PFGMN; PFC00006; ABC_tran; I.
SWART; SM0382; AAA, I.
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Q81G51;
                                                                                                                                                                                                                       Best Local Similarity 53.9
Matches 160; Conservative
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65 CGHSIRSEREKALEQIGAIVENPELYDYMTGMQNLKHFANMAITPISKERIABIVKLVEL 124
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                           Gaps
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07-FEB-2006, entry version 14.
ARC transporter, APP-binding protein; possible bacitracin transport ATP-binding protein.
OrderedLocusNames=BED727, 5081;
Bacillus thuringiensis subsp. konkukian.
Bacieria, Firmicutes; Bacillales; Bacillus;
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                                                                                                                                                                              10;
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Complete_proteome; Nucleotide-binding; Transport.
SEQUENCE 300 AA; 33300 MW; BFC416D41D47E21B CRC64;
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                                                                                                                  50.6%; Score 781; DB 2; Length 300;
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48.2%; Pred. No. 1.3e-34;
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PROSITE; PS50893; ABC_TRANSPORTER_2; 1
                                                                                                                                                4.2e-36;
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                                                                                                                        Query Match
Best Local Similarity 53.44
Matches 159; Conservative
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NCBI TaxID=180856;
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EMBL/GenBank/DDBJ databases.

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Q3EW61_BACTI
Q3EW61;
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Best Local 9
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X PULLEOLIDE SAQUENCE LAWGES SCALE GENOMIC DNAJ.

X REDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;

A REDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;

A Read T.D., Peterson S.N., Tourasse N.J., Baillat.E.W., Faulsen I.T.,

A Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., W.M.,

A Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,

A Benton J.L., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,

Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,

A Berty K.J., Platut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,

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Salzberg S.L., Thomason B., Friedlander A.M., Kohler T.M.,

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The genome sequence of Bacillus anthracis Ames and comparison to Closely related bacteria.";

L. Nature 423:81-86(2003).
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EENMSVFISSHLLSEVQMICDRVAIIHKGKMITVAKV-----EELIKTASDRVEWIVT
                           LETLLELKNVSKTIRGKKI I EGLSFDVRAGEI FGFLGPNGAGKTTTIRMI VGHMSITAGE
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                                                                                   61 IAVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELV
   Gaps
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 17;
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QBIJQ2; Q6HQ9B;
QBIJQ2; Q6HQ9B;
QBIJQ2; Q6HQ9B;
QBIJQN-2003, integrated into UniProtKB/TrEMBL.
O1-UN-2003, sequence version 1.
O7-FRB-2006, entry version 20.
ABC transporter, ATP-binding protein.
OrderedLocupNames=BAS650, BAS5252, GBAAS650; ORFNames=BA_S650;
 76; Indels
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Bacillus cereus group.
NCBI_TaxID=1392;
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69; Mismatches
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151; Conservative
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                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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Anderson I., Sorokin A., Kapatral V., Reznik G., Bhattacharya A.,
Mikhailova N., Burd H., Joukov V., Kaznadzey D., Walunas T.,
D'Souza M., Larsen N., Pusch G., Liolios K., Grechkin Y., Lapidus A.,
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PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Complete proteones; Nucleotide-binding; Transport.
SEQUENCE 305 Ab; 34399 WW; 6412E2488BA6C24A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 305;
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07-FFB-2006, entry version 4.
Bacitracin transport ATP-binding protein bcrA.
ORPNames-REHT, 05356;
Bacillus thurIngiensis serovar israelensis ATCC 35646.
Baceria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
ubmitted (MAY-2004) to the EMBL/GenBank/DDBJ databases
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EMBL; AE017225; AAT57540.1; -; Genomic DNA.
EMBL; AE017334; AAT70166.1; -; Genomic DNA.
                                                                                                                                                                                                                                                                          TIGR; GBAA5650; -.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016887; F:ATPase activity; IEA.
GO:0000166; F:Mucleotide binding; IEA.
GO; GO:0006810; P:transport; IEA.
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InterPro; IPR003439; ABC_transp_like.
Pfam; PF00005; ABC_tran; 1.
ProDom; PD00006; ABC_transporter; 1.
SMART; SM00382; AAA; 1.
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NCBI_TaxID=339854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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61 IAVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELV 120
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Distributed under the Creative Commons Attribution-NoDerivs License
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                              PubMed=14960714; DOI=10.1093/nar/gkh258;
Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
Shores K.A., Fouts D.E., Tourasse N.J., Angluoli S.V., Kolonay J.F.,
Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
"The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
adaptetions and a large plasmid related to Bacillus anthracis pXOl.";
Nucleic Acids Res. 32:977-988(2004).
-: SIMILARITY: Belongs to the ABC transporter family.
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PROSITE; PSG0893; ABC_TRANSPORTER_2; ATP-binding; Complete protecome; Nucleotide-binding; Transport.
SEQUENCE 305 AA; 34406 MW; FDEEA942E1DFF99A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.2%; Score 743.5; DB 2; Length 305; 47.8%; Pred. No. 5.5e-34; Live 68; Mismatches 77; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .5e-34;
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   SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AE017194; AAS44429.1; -; Genomic_DNA.GO; GO:0005524; F:ATP binding; IEA.GO; GO:001689; F:ATP binding; IEA.GO; GO:000166; F:nucleotide binding; IEA.InterPro; IPR003593; AAA_ATPase.InterPro; IPR003439; ABC_transp_like.Pfam; PF00005; ABC_transp_like.Propom; P000006; ABC_transp_like.Propom; SNO00006; ABC_transporter; 1.
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PubMed=15155910; DOI=10.1073/pnas.0402414101;
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Q4MLR2;
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Matches 150; Conservative
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NCBI_TaxID=269801;
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                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Goltsman E., Chu L., Fonstein M., Ehrlich D., Overbeek R., Kyrpides N., Ivanova N.;
"Comparative genome analysis of Bacillus cereus group genomes with Bacillus subtilis ";
submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
-!- SIMILARITY: Belongs to the ABC transporter family.
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Bacteria, Firmicutes, Bacillales, Bacillus, Bacillus cereus group.
NCBI_TaxID=222523;
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                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AAJM01000065; EAOS5544.1; -; Genomic_DNA. GO; GO:0005524; F:ATP binding; IEA. GO; GO:0016897; F:ATPabee activity; IEA. GO; GO:000166; F:nuclectide binding; IEA. GO; GO:000610; P:transport; IEA. InterPro; IPR00359; AAA_ATPase. InterPro; IPR003033; ABC transplike. InterPro; IPR002048; EF_hand_Ca_bd. Probom; PD000005; ABC transplike. Probom; PD000006; ABC transporter; 1. SM00382; AAA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PSO0211; ABC_TRANSPORTER_1; UNKNOWN_1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
PROSITE; PS00191; BF HAND 1; UNKNOWN 1.
PROSITE; PS001018; BF HAND 1; UNKNOWN 1.
SEQUENCE 305 AA; 34330 WW; CASO06F148498EEC
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07-FRB-2006, entry version 13.
ABC transporter, ATP-binding protein.
ORRNames-ECE_5529;
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Q72X49;
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238 LTREABAPERKVKVDEAEGGIELSIQKD--EVPDLIKHLTDSGVRLYEVKAVNKSLEDRFL 295
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Distributed under the Creative Commons Attribution-NoDerivs License
Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D., Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W., Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z., Rilstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D., Popovic T., Fraser C.M.;
"Identification of anthrax toxin genes in a Bacillus cereus associated with an illness resembling inhalation anthrax.";
Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
-! CAVTION: The sequence shown here is derived from an EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
-! SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapa
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. 48.0%; Score 739.5; DB 2; Length 305;
Best Local Similarity 47.6%; Pred. No. 9.2e-34;
Matches 147; Conservative 68; Mismatches 85; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
PROSITE; PS00018; BF HAND 1; UNKNÖWN 1.
ATP-binding; Nucleotide-binding; Transport.
SEQUENCE 305 AA; 34399 MW; B61CD34B61FC2C48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AAEKO1000030; EAL13109.1; -; Genomic_DNA. GO; GO:0005524; F.ATP binding; IEA. GO; GO:0005524; F.ATP binding; IEA. GO; GO:00166; F:nucleotide binding; IEA. GO; GO:000616; F:nucleotide binding; IEA. INTERPRETO: IPRO0359; AAA ATPASE. InterPro; IPR003439; ABC_transp_like. InterPro; IPR003439; AEC_transp_like. Feam; PF00005; AEC_transp_like. Fram: PF00005; AEC_transporter; I. ProDom; PD000006; AEC_transporter; I. ProDom; PD000006; AEC_transporter; I.
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Search completed: July 13, 2006, 13:49:00 Job time : 301 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

July 13, 2006, 13:49:18; Search time 50 Seconds (without alignments) 537.438 Million cell updates/sec Run on:

1 LETLLELKNVSKTIRGKKII......KSLEDRFLEITADKEEAQHV 307 US-10-510-941-2 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

650591 segs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

lesued Patents AA:*
l: /BMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:*
l: /BMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:*
l: /BMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:*
l: /BMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:*
l: /BMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:*
l: /BMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:*
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l: /BMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:*
l: /BMC Celerra SIDS3/ptodata/2/iaa/RE

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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-	455.5	29.5	310	~	US-09-107-532A-6910	Sequence 6910, Ap
~	436	28.3	233	~	US-09-627-376-12	
ო	436	28.3	233	~	US-10-047-676B-12	Sequence 12, Appl
4	430.5	27.9	332	~	US-09-107-532A-3752	
'n	416.5	27.0	303	~	US-09-107-532A-5192	
9	410	26.6	345	7	US-09-252-991A-31957	
7	408.5	26.5	330	~	US-09-902-540-15345	
æ	407.5	26.4	319	~	US-09-758-759-89	Sequence 89, Appl
σ	397	25.7	328	~	US-09-902-540-10796	
10	396.5	25.7	309	~	US-09-252-991A-21204	
11	392.5	25.5	215	~	US-09-583-110-2846	
12	392.5	25.5	229	~	US-09-107-433-3116	•
13	391.5	25.4	309	~	US-09-902-540-16586	
14	384.5	24.9	228	~	US-09-602-787A-402	
15	381	24.7	788	~	US-09-252-991A-28171	Sequence 28171, A
16	374.5	24.3	240	~	US-09-902-540-15786	
17	373	24.2	292	~	US-09-602-787A-352	Sequence 352, App
18	371.5	24.1	290	~	US-09-902-540-16248	16248,
19	371.5	24.1	594	~	US-09-543-681A-5528	
50	367	23.8	588	~	US-09-489-039A-13579	13579,
21	363.5	23.6	315	N	US-09-134-000C-6449	Sequence 6449, Ap
22	362.5	23.5	245	~	US-09-902-540-13001	13001,
23	354.5	23.0	248	~	US-09-710-279-3218	Sequence 3218, Ap
24	352.5	22.9	316	~	US-09-902-540-10994	10994,
25	349.5	22.7	1272	~	US-09-949-016-7472	7472,
56	347.5	22.5	2059	٣	US-10-114-270-176	Sequence 176, App

NAME/KEY: misc feature LOCATION: (B) LÖCATION 1...310 SEQUENCE DESCRIPTION: SEQ ID NO: 6910:

FEATURE

27 347.5 22.5 2144 2 US-10-154-419-2 Sequence 2, Appli 2 346.5 22.5 146 2 US-09-949-016-6947 Sequence 25, Appli 3 46.5 22.5 1684 2 US-08-765-520-25 Sequence 25, Appli 3 46.5 22.5 1684 2 US-08-765-520-25 Sequence 25, Appli 3 346.5 22.5 1704 2 US-09-762-500-75 Sequence 120, Appli 3 346.5 22.5 1704 2 US-09-762-500-75 Sequence 75, Appli 3 346.5 22.5 1704 2 US-09-105-107-5324-5424 Sequence 120, Appli 3 346.5 22.4 304 2 US-09-107-532A-5424 Sequence 120, Appli 3 346.5 22.3 27.2 US-09-107-532A-4981 Sequence 4766, Appli 3 341 2 2.1 254 2 US-09-107-532A-4981 Sequence 4766, Appli 3 341 2 2.1 254 2 US-09-107-532A-4981 Sequence 4766, Appli 3 341 2 2.1 254 2 US-09-107-532A-4981 Sequence 4205, Appli 3 341 2 2.0 3 27 2 US-09-107-532A-4981 Sequence 7592, Appli 3 3 2 2 0 3 2 US-09-107-433-792 Sequence 7592, Appli 3 3 2 2 0 3 2 US-09-107-433-331 Sequence 3 3 3 3 3 3 4 4 5 2 1 2 US-09-107-433-331 Sequence 3 3 3 3 3 4 5 2 1 7 2 US-09-107-438-8 Sequence 3 3 3 3 4 4 5 2 1 7 2 US-09-107-438-3 Sequence 3 3 3 4 4 5 2 1 7 2 US-09-107-438-3 Sequence 3 3 3 4 4 5 2 1 7 2 US-09-107-438-3 Sequence 3 3 3 4 4 5 2 1 7 2 US-09-107-438-3 Sequence 3 3 3 4 4 5 2 1 7 2 US-09-107-438-3 Sequence 3 3 3 4 4 5 2 1 7 2 US-09-107-438-3 Sequence 3 3 3 4 4 5 3 3 4 5 5 1 7 2 US-09-107-438-3 Sequence 3 3 3 4 4 5 3 3 4 5 5 1 7 2 US-09-107-438-3 Sequence 3 3 3 4 4 5 3 3 4 5 5 1 7 2 US-09-107-438-3 Sequence 3 3 3 4 4 5 3 3 4 5 5 1 7 2 US-09-107-438-3 Sequence 3 3 3 4 4 5 3 3 4 5 5 1 7 7 2 US-09-107-438-3 Sequence 3 3 3 4 4 5 3 3 4 5 5 1 7 7 2 US-09-107-438-3 Sequence 3 3 3 4 4 5 3 3 4 5 5 1 7 7 2 US-09-107-438-3 Sequence 3 3 3 4 4 5 3 3 4 5 5 1 7 7 2 US-09-107-438-3 Sequence 3 3 3 4 4 5 3 3 4 5 5 1 7 7 2 US-09-107-438-3 Sequence 3 3 3 4 4 5 3 3 4 5 5 1 7 7 2 US-09-107-438-3 Sequence 3 3 3 4 4 5 3 3 4 5 5 1 7 7 2 US-09-107-438-3 Sequence 3 3 3 4 4 5 3 3 4 5 5 1 7 7 2 US-09-107-438-3 Sequence 3 3 3 4 4 5 3 3 4 5 5 1 7 7 2 US-09-408-408-408-408-408-408-408-408-408-408
22.5 2144 2 US-10-154-419-2 22.5 2146 2 US-09-949-016-6947 22.5 1684 2 US-08-655-259-25 22.5 1684 2 US-08-655-259-25 22.5 1704 2 US-08-762-500-75 22.5 1704 2 US-09-762-500-75 22.5 1766 2 US-09-919-016-10796 22.4 304 2 US-09-107-532A-5424 22.3 607 2 US-09-107-532A-5424 22.1 254 2 US-09-107-532A-4065 22.1 254 2 US-09-107-532A-4065 22.1 254 2 US-09-107-532A-4205 22.0 259 2 US-09-107-532A-4205 22.0 317 2 US-09-107-532A-4205 22.0 323 2 US-09-107-532A-4205 22.0 323 2 US-09-107-532A-4205 22.0 327 2 US-09-328-322-7592 22.0 327 2 US-09-328-3131 22.0 327 2 US-09-328-3131 22.1 317 2 US-09-328-3131
22.5 2144 2 22.5 1684 2 22.5 1684 2 22.5 1684 2 22.5 1704 2 22.5 1704 2 22.3 1704 2 22.3 267 2 22.3 267 2 22.1 291 2 22.0 323 2
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22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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Sequence 6910, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                          NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <UNKNOWN>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: AFINICATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (781)893-507
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6910:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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RESULT 1
US-09-107-532A-6910
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US-10-047-676B-12
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                                                                                                2 ETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEI
                                                                                                                   LKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTRE
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                                                                Gaps
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                               Length 310;
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GENES AND PROTEINS
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                                                              Indels
                      29.5%; Score ... 7.2e-v.,
34.6%; Pred. No. 7.2e-v.,
...a 79; Mismatches 107;
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28.3%; Score 436; DB 2;
Best Local Similarity 41.5%; Pred. No. 3.7e-34;
Matches 93; Conservative 51; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/09627376

Sequence 12, Application US/09627376

Patent No. 6142308:
GENERAL INFORMATION:
TITLE OF INVENTION: WUTAZIN I BIOSYNTHESIS GENI
TITLE OF INVENTION: WUTAZIN I BIOSYNTHESIS GENI
CURRENT APPLICATION NUMBER: US/09/627,376
CURRENT FILING DATE: 2001-05-30

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PATENTIN VETSION 3.0

SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Streptococcus mutans US-09-627-376-12
                                                              Matches 104; Conservative
                                             Best Local Similarity
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US-09-107-532A-6910
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Sequence 12, Application US/10047676B

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RESULT 4
US-09-107-532A-3752
i Sequence 3752, Application US/09107532A
j Sequence 3752, Application US/09107532A
j Patent No. 6583275
j GENERAL INFORMATION:
j TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
j TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 JAVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ILIDG---HDWSRKDLENIGALIESPPLYENLTARENLKVRTLML-GLPDSRIDEVLKIV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GLKNRINDKVKTYSLGMRORLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MDYMLETKNLTKQFGKQTAVNQLNLKVERHSIYGLLGPNGSGKSTTLKMITGMLRKTSGH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGE
GREATAL INFORMATION:
GREATAL INFORMATION:
APPLICANT: Qi, Fengia
APPLICANT: Caufield, Page W.
APPLICANT: Chen, Ping
TILLE BEFERENCE: UAB-17403/22
CURRENT FILING DATE: 2002-01-14
CURRENT FILING DATE: 2002-01-14
FRICA APPLICANTON NUMBER: US Q) 627,376
FRICA REPERINGE: 2000-07-28
FRICA APPLICATION NUMBER: US Q) 627,376
FRICA APPLICATION NUMBER: US D) 627,376
FRICA APPLICATION NUMBER: US SQFTWARE: PALENTING DATE: 2000-07-28
FRICA APPLICATION NUMBER: US SQFTWARE: PALENTING DATE: 2000-07-28
FRICA APPLICANTON NUMBER: US SQFTWARE: PALENTER: 2000-07-28
FRICA A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 EKGMAVIVSSHLLSEMELMCDRIALIQNGKLRDIQHVHGPARDE 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.3%; Score 436; DB 2;
41.5%; Pred. No. 3.7e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Famela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Sequence 31957, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PLICATION NUMBER: US 60/074,788
PRIOR PLICATION NUMBER: US 60/074,788
PRIOR PELICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 ENEISPSSHKGLEQVGALIEXPGIYPFLTGYDHLKLFSE-TNDVS--AIDTIVNQLKMEK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 GVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELVGLKN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 RINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKGM 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 AVIVSSHLLSEMELMCDRIALIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTREAAA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 FRKVKVDEAEGGIELSIQKDEVPDLIKHLTDS------GVRLYEVKAVNKSL 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 LSVQELSKNFGHKQALSDVSFSLSPGKIVGLVGPNGAGKTTIMKAILGLIHYSDGTICIG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 LELKAVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVC
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27.0%; Score 416.5; DB 2;
Best Local Similarity 33.6%; Pred. No. 4.3e-32;
Matches 103; Conservative 62; Mismatches 109;
                                                                                       NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-507
INFORMATION FOR SEQ ID NO: 5192:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...303

SEQUENCE DESCRIPTION: SEQ ID NO: 5192:

US-09-107-532A-5192
                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Enterococcus faecium
FILING DATE: 14 May 1998
APPLICATION UNDRER: 60/051571
FILING DATE: JULY 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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LENGTH: 345
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 CGVSVKENFEKAARHIGAIVENPELYKFLTGYONL---QQYARMTKGVTKKKIDEIVELV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAAAFRKVKVDEAE----GGI----BLSI-----OKDEVPDLIKHLTDSGVRLYEVKAVNK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 EIVFFSKKEREOFEELLPGGMIRSELRIAYPQKSKEEMLFAMDLLAKYQLPVQSVQMEEP 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 332;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.9%; Score 430.5; DB 2; Best Local Similarity 35.9%; Pred. No. 2.1e-33; Matches 111; Conservative 60; Mismatches 109;
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SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...332
SEQUENCE DESCRIPTION: SEQ ID NO: 3752:
US-09-107-532A-3752
                                                                                                                                                                                                                                                           ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/085,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
              TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3752:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5192, Application US/09107532A Patent No. 6581275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 100 Beaver Street
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Waltham
STATE: Massachusetts
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                                                                                                                                                                                                                                   ORIGINAL SOURCE:
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56 ITAGEIAVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTK----K 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 RDYLRKLTREKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 ADDTQALTREAAAFRK-----VKVDEAEGGIELSIQKDE----VPDLIKHLTDSGVRLYE 282
                 224 EKKRYYIQADDTQALTREAAAFRKVKVDEAEGGIELSIQKDE--VPDLIKHLTDSGVRLY 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10796, Application US/09902540
; Sequence 10796, Application US/09902540
; Septemt No. 683347
; GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Stewen C.
; APPLICANT: Misgand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 LLELKNVSKTIRGK-----KIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMS
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26.4%; Score 407.5; DB 2; Length
Best Local Similarity 32.0%; Pred. No. 3.4e-31;
Matches 101; Conservative 65; Mismatches 125; Indels
                                                                                                                                                                                                                                                                     Sequence 89 Application US/09758759
Fatent No. 6861513
GENERAL INFORMATION:
APPLICANT: HOSTEN, Time X.
TITLE OF INVENTION: Everninomicin Biosynthetic Genes
TITLE OF INVENTION: Everninomicin Biosynthetic Genes
FILE REFERENCE: ID0993X US
CURRENT FILING DATE: 2001-01-11
FRIOR PELING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 204
SOFTWARE OF SEQ ID NOS: 204
SOFTWARE PATENTINOM NOW TITLE
SOFTWARE OF SEQ ID NOS: 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Micromonospora carbonacea
                                                                                                                                                           295 SVALRRPTLADVFLOLT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 VKAVNKSLEDRFLEIT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 IELHRPSLDDVFLTKT 312
                                                                                                                 282 EVKAVNKSLEDRFLEIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: evbC
US-09-758-759-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-09-902-540-10796
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US-09-758-759-89
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                                                                   244
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Sequence 15345, Application US/09902540

Patent No. 683347

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Glater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

TITLE OF INVENTION: Myxococcue xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15449)B

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 15345
                                                                                                                      9
                                                                                                                                                                                                                                                             62 AVCGVSVKENFEKAARHIGAIVENPELY-----KFLTGYQNLQQYARMTKGVTKKKIDE 115
                                                                                                                                                                                                                                                                                                   96 RIFGFDMQDKARQAQKLIGYLPENAPSYGEMIVEGFLAFVASIRDYSGREK---RRRIDS 152
                                                                                                                                                                                                                                                                                                                                                          116 IVELVGLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYL 175
                                                                                                                                                                                                                                                                                                                                                                                      153 AMDCMELRDERRSIIETLSKGFKRRVALAQAILHDPELLLLDEPTDGLDPNQKHQVRQLV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 RKLTREKGMAVIVSSHLLSEMELMCDRIAJIQNGKLRDIQHVHGPARDEKKRYYIQADDT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| | | : : | | |: BAPUDPLAIAMLPGVAGIEGRPDRAGILTILARPGVQI-----LPALNRLIHGSGWRVS 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 AVCGVSVKENFEKAARHIGAIVENPELYKFLIGYONLOQYARMIKGV----TKKKIDEIV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 ELVGLKNRINDKVKTYSLGMRQRLGLAOSLLHDPKLLILDEPTNGLDPAGIREIRDYLRK 177
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                                                                                                                                                                                            2 ETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEI
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                                                                                                                      Gaps
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                                                                      Length 345
                                                                   Query Match 26.6%; Score 410; DB 2; Length 34 Best Local Similarity 29.5%; Pred. No. 2.2e-31; Matches 94; Conservative 77; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71; Mismatches 109; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 EVKAVNKSLEDRFLEITAD 300
j ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31957
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Sequence 2846, Application US/09583110

Sequence 2846, Application US/09583110

Patent No. 6699703

GENERAL INFORMATION:

APPLICATOR: Lynn Doucette-Stamm et al.

ITILE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcu

ITILE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 1998-06-26

PRIOR PILING DATE: 1998-06-12

PRIOR PILING DATE: 1998-05-12

PRIOR PILING DATE: 1998-05-12

PRIOR PILING DATE: 1999-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 2846
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                                                                                                         KKIDEIVELVGLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIRE 170
                                                                                                                                                                                           122 LELDEV------RQTIETLSKGFRRVGLAQAILHEPRALVLDEPTDGLDPNQKHQ 172
                                                                                                                                                                                                                                                                                                                                                                     227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 IFGFDIRNRTLQAQRLIGYLPEGSPCYAEMTVQGFLDFIAEIRGYRGAGKRERVARALGL 121
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                     171 IRDYLRKLTREKGMAVIVSSHLLSEMELMCDRIAIIQNGK-LRDIQHVHGPARDEKKRYY
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Patent No. 6800744
GENERAL INFORMATION:
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Patent No. 6551795

GENERAL INFORMATION:

Patent No. 6551795

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ABENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPREBRUCE: 107196.136

CURRENT PILING DATE: 1999-02-18

PRIOR PILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.7%; Score 397; DB 2; Length 32: Best Local Similarity 31.0%; Pred. No. 3.7e-30; Matches 101; Conservative 72; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 25.7%; Score 396.5; DB 2; Similarity 30.0%; Pred. No. 3.8e-30; 98; Conservative 71; Mismatches 111;
FILE REFERENCE: 38-10(15849)B
CURRENT PEDICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 10796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTDSGVRLYEVKAVNKSLEDRFLEIT 298
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                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Myxococcus xanthus
US-09-902-540-10796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-991A-21204
                                                                                                                                                                                                                                                                                                                  LENGTH: 328
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Best Local S
Matches 98
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64 CGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKK----KIDEIVEL 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 VGLKNRINDKVKTYSLGMRORLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 REKGM-AVIVSSHLLSEMELMCDRIALIQNG------KLRDIQHVHGPARDEK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SCH"der, Hartwig
APPLICANT: SCH"der, Hartwig
APPLICANT: SCH"der, Hartwig
APPLICANT: Sch"der, Cokar
APPLICANT: Sch"der, Cokar
APPLICANT: Alberhauer, GFEGOR
TITLE OF INVENTION: CORYNBBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: TRANSPORT
TITLE OF INVENTION: TRANSPORT
FILE REFERENCE: BG1-125CP
CURRENT FILING DATE: 1090-06-23
CURRENT FILING DATE: 1090-06-25
FRIOR APPLICATION NUMBER: USN 60/141031
PRIOR APPLICATION NUMBER: DE 19931454.3
FRIOR APPLICATION NUMBER: DE 19931478.0
FRIOR FILING DATE: 1999-07-08
FRIOR FILING DATE: 1999-07-08
FRIOR FILING DATE: 1999-07-08
FRIOR RELICATION NUMBER: DE 1993122.1
FRIOR APPLICATION NUMBER: DE 1993122.1
FRIOR FILING DATE: 1999-07-09
FRIOR APPLICATION NUMBER: DE 19932125.6
FRIOR FILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 KRYYIQADDTQALTREAAAFRKVKVDEAEGG-IELSIQ--KDEVPDLIKHLTDSGVRLYE 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 AR-----AVEVLOR----FGSVEVDRASDGLVALTVRASPDORPQVAOAVVGAGLELLR 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                              35;
                                                                                                                                                                                                                                                                                                                                                        Length 309;
                                                                                                                                                                                                                                                                                                                                                   Query Match
25.4%; Score 391.5; DB 2; Length 3
Best Local Similarity 32.8%; Pred. No. 1.2e-29;
Matches 105; Conservative 62; Mismatches 118; Indels
     ; TITLE OF INVENTION: Myxococcus xanthus Genom
FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; LENGTH: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 402, Application US/09602787A Patent No. 6696561 GENERAL INFORMATION: APPLICANT: Pempejus, Mark APPLICANT: Kr"ger, Burkhard APPLICANT: Sch"der, Hartwig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 VKAVNKSLEDRFLEITADKE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287 LDOGAGOLESIFLRLTHGOE 306
                                                                                                                                                                                                                                                                         , ORGANISM: Myxococcus xanthus US-09-902-540-16586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-602-787A-402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 GLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDBPTNGLDPAGIREIRDYLRKLTR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 MNEIITLKNIELKLKKKTCVPQNLNFSCKQGEIIGITGANGSGKSVLFKLIAGLYSPSYGE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LETLLELKANVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGE
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           NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESSE:
ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.5%; Score 392.5; DB 2; Best Local Similarity 33.7%; Pred. No. 6e-30; Matches 70; Conservative 62; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...229
; SEQUENCE DESCRIPTION: SEQ ID NO: 3116:
US-09-107-433-3116
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 EKGMAVIVSSHLLSEMELMCDRIAIIQN 208
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EKGTTILIASHSEDIRILCDKVYAIED 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16586, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
                                                                                                                                                                                                   ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (701) 893-8277
INFORMATION FOR SEQ ID NO: 3116:
SEQUENCE CHARACTERISTICS:
LENGTH: 229 amino acid
                                                                                                                                                   STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                         CITY: Waltham
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RESULT 15
US-09-252-991A-28171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV 63
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24.9%; Score 384.5; DB 2;
Best Local Similarity 41.2%; Pred. No. 3.6e-29;
Matches 87; Conservative 45; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-04
PRIOR PILING DATE: 1999-07-04
PRIOR PILING DATE: 1999-08-27
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-09-31
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US-09-602-787A-402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
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Sequence 28171, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-07-17
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28171
LENGTH: 788
                                  121 GLKARINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 KNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 AAFRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEITADKE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 GMAVIVSSHLLSEMELMCDRIALIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTREA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 VCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

24.7%; Score 381; DB 2; Length 786

Best Local Similarity 31.8%; Pred. No. 4.9e-28;

Matches 97; Conservative 57; Mismatches 111; Indels
                                                                                                                                              181 EKGMAVIVSSHLLSEMELMCDRIALIQNGKL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ::: ||:| :| || || ||:|:
GTGIVLCSHVLPGVETHIDRAAILAGGRLQ-
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he: 52 secs
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28171
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1502, Ap 10399, A 11165, Ap 6521, Ap 16655, Ap 1202, Ap 1771, Ap 11149, A 11149, A 3029, Ap 3029, App 1166, Ap 11149, A 11262, App

OM protein

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Sequence:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Sequence 2, Application US/10510941
| Sequence 2, Application US/10510941
| Publication No. US20060040346A1
| GENERAL INFORMATION:
| APPLICANT: Jorgensen, Steen Troels
| APPLICANT: Raemussen, Michael Dolberg
| APPLICANT: Raemussen, Jens Tonne
| APPLICANT: Andersen, Jens Tonne
| APPLICANT: Clausen, ID Groth
| TITLE OF INVENTION: Improved Bacillus Host Cell
| FILE REFERENCE: 10297.204-US
| CURRENT APPLICATION WUMBER: US/10/510,941
| CURRENT FILING DATE: 2004-10-08
| NUMBER OF SEQ ID NOS: 22
| SEQ ID NO SEQ ID NOS: 22
| SEQ ID NO SEQ ID NOS: 33
| SEQ ID NO SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 100.0%; Score 1542; DB 5; Local Similarity 100.0%; Pred. No. 6.9e-123; NB 307; Conservative 0; Mismatches 0;
US-10-732-923-1502
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US-10-156-761-10399
US-10-369-493-11165
US-10-738-626-6521
US-10-738-626-6521
US-10-369-493-16655
US-10-369-493-1202
US-10-369-493-1202
US-10-732-923-1771
US-10-732-923-1537
US-10-369-493-1149
US-10-369-493-1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Bacillus licheniformis
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Best Local S:
Matches 307,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Appli
Sequence 16618, A
Sequence 60404, A
Sequence 182, App
Sequence 885, App
Sequence 84, Appl
                                                                                                                                                                                                                      July 13, 2006, 13:49:57 ; Search time 186 Seconds (without alignments) 764.554 Million cell updates/sec
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1542
1 LETLLELKNVSKTIRGKKII.......KSLEDRFLEITADKEEAQHV 307
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                                  GenCore version 5.1.9
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US-10-282-122A-52344
US-10-369-493-18115
US-10-369-493-18754
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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491.5
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Gaps

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300

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COSSART, PASCALE
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                                                                 APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)8
CURRENT FILING NATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2003-02-21
PRIOR PLILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 16618
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                81;
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                   Sequence 16618, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bacillus thuringiensis US-10-369-493-16618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ollsen, Kari
APPLICANT: Ollsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Tanick, John
APPLICANT: Yamamoto, Robert
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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10-369-493-16618
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62 AVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELVG 121
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CURRENT FILING DATE: 2003-02-20

FRICA FILING DATE: 2000-03-21

FRICA FILING DATE: 2000-03-21

FRICA FILING DATE: 2000-05-23

FRICA FILING DATE: 2000-05-23

FRICA FILING DATE: 2000-05-23

FRICA FILING DATE: 2000-05-26

FRICA FILING DATE: 2000-05-26

FRICA FILING DATE: 2000-09-09

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FRICA FILING DATE: 2000-09-09

FRICA FILING DATE: 2000-10-23

FRICA FILING DATE: 2000-10-23

FRICA FILING DATE: 2000-12-22

FRICA FILING DATE: 2000-10-03-09

FRICA FILING DATE: 2000-12-22

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47.6%; Score 734; DB 4; Length 301;
Best Local Similarity 49.8%; Pred. No. 4.8e-54;
Matches 149; Conservative 61; Mismatches 81; Indels
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APPLICANT: FRANGEUL, LIONEL
APPLICANT: COUVE, ELISABETH
APPLICANT: NCONICK, CHRISTOPHE
APPLICANT: DEHOUX, PIERRE
APPLICANT: DEHOUX, PIERRE
APPLICANT: DEHOUANI, FARID
APPLICANT: NEDARRI, HARED
APPLICANT: GHASER, PHILIPPE
APPLICANT: GLASER, PHILIPPE
APPLICANT: GLASER, PHILIPPE
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US-10-282-122A-60404
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US-11-045-004-182
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GARCIA DEL PORTILLO, FRANCISCO
GOMEZ-LOPEZ, NURIA
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CHARBIT, ALAIN
DURANT, LIONEL
PEREZ-DIAZ, JOSE-CLAUDIO
BAQUERO, FERNANDO
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GARRIDO-GARCIA, PATRICIA
TIERREZ-MARTINEZ, ALBERTO
                                                                 Sequence 885, Application US/11045004
Publication No. US20060078901A1
GENERAL INFORMATION:
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COUTE, ELISABETH
RUSNIOK, CHRISTOPHE
FSIHI, HAPIDA
DENOUX, PIERRE
DUSSURGET, OLIVER
CHETOUANI, FARID
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KARST, UWE
ENITAN, KARL-DIETER
HAUF, JORG
ROSE, MATTHIAS
VOSS, HAMUT
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DANIELS, JUSTIN
GOEBEI, WERNER
KREFT, JURGEN
KUHN, MICHAEL
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PABLOS, BETRIZ DE
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GLASER, PHILIPPE
KUNST, FRANCK
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HAIN, THORSTEN
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APPLICANT: VOSS, HAMUT
ITILE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
FILE REFERENCE: 05394.0018-02
CURRENT PELICON NUMBER: US/11/045,004
CURRENT PELICON NUMBER: US/11/045,004
CURRENT PELICON NUMBER: US/11/045,004
FRIOR PELICATION NUMBER: 10/637,657
FRIOR FILING DATE: 2003-08-11
FRIOR FILING DATE: 2001-04-11
FRIOR FILING DATE: 2001-04-11
FRIOR APPLICATION NUMBER: PCT/PR01/01118
FRIOR PELICON STELL SO01-04-11
FRIOR FILING DATE: 2000-04-11
FRIOR FILING DATE: 200
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BAQUERO, FERNANDO
GARCIA DEL PORTILLO, FRANCISCO
                                                                                                                                               VAZQUEZ-BOLAND, ANTONIO
DOMINGHEZ-BERNAL, GUSTAVO
GARRIDO-GARCIA, PATRICIA
TIERREZ-MARTINEZ, ALBERTO
AMEND, ALEXANDRA
CHAKRABORTY, TRINAD
DOMANN, EUGEN
HAIN, THORETEN
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; ORGANISM: Listeria monocytogenes
US-11-045-004-182
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KARST, UWE
ENTIAN, KARL-DIETER
HAUF, JORG
ROSE, MATTHIAS
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MADUENIO, ENCARNA
PABLOS, BETRIZ DE
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CHARBIT, ALAIN
DURANT, LIONEL
DANIELS, JUSTIN
                                                                    CREFT, JURGEN KUHN, MICHAEL
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APPLICANT:
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2 ETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEI 61 TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES THIE REPRENRINCE: 05394.0018-02 CURRENT APPLICATION NUMBER: US/11/045,004 CURRENT FILING DATE: 2005-01-28 Gaps ~ Query Match 41.4%; Score 639; DB 6; Length 306; Best Local Similarity 45.3%; Pred. No. 6.1e-46; Matches 135; Conservative 57; Mismatches 104; Indels PRIOR PELLING DATE: 2003-01-25.
PRIOR FILING DATE: 2003-08-11
PRIOR PELLING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: 10/257,023
PRIOR PILING DATE: 2002-10-08
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 2854
SOFURDE: PATENTING DATE: 2005-04-11
NUMBER OF SEQ ID NOS: 2854
SOFURD NOS: 2854
LENGTH: 306

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Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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185 AVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARD-EKKRYYI----QADDTQALT 239
                                                                              GLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR 180
                                                                                                    123 KLTGAINQKVKTYSLGMRQRLGVAQALIHSPALLILDEPTNGLDPQGMAEFRTLIRDLA- 181
                                                                                                                                                          181 EKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTR 240
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                                                                                                                                                                                   182 TNGTSVLISSHLLSEIQQITDRPAIINKGVLTHIEKMSDLIENHVAAYKLKVSDPVATTT 241
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                                                                                                                                                                                                                                                               240 REAAAFRKVKVDEAEGGIELSIOKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEI 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91; Indels
                                                                                                                                                                                                                                                                                                                                                                      Sequence 84, Application US/10510386
Publication No. US20050244922A1
GENERAL INFORMATION:
APPLICANT: Andersen, Jens Tonne
APPLICANT: Andersen, Jens Tonne
APPLICANT: Clausen, Ib Groth
APPLICANT: Olsen, Peter Bjarke
APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: Improved Bacillus Host Cell
FILE REPRENCE: 10294.204-US
CURRENT APPLICATION NUMBER: US/10/510,386
CURRENT FILING DATE: 2004-10-04
CUNBER FILE OF SEQ ID NOS: 248
CURRENT FILING DATE: 2004-10-04
CURRENT FILING DATE: 2004-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66; Mismatches
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; Sequence 73352, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Bacillus licheniformis US-10-510-386-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 44.0%
Matches 131; Conservative
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APPLICANT: Wang, Liangsu APPLICANT: Zamudio, Carlos APPLICANT: Malone, Cherryl APPLICANT: Haselbeck, Robert

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APPLICANT: Xu, H.

TITLE OF INVENTION:
CURRENT APPLICANT:
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-66
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-04
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34.8%; Score 536; DB 4; Length 302;
Best Local Similarity 39.3%; Pred. No. 3.6e-37;
Matches 116; Conservative 64; Mismatches 111; Indels
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Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Streptococcus mutans US-10-282-122A-72352
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION C
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(5205.2)
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                       80 VGSLIESPSYYGHLSGYENLRIIATL-KGTPEKDIGRVLEIVRLENQKNKKTNQYSLGMK 138
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Sequence 20363, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:
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US-10-369-493-1297
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
                                                                          g
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR RILING DATE: 2002-02-21
SRQ ID NOS: 47374
SRQ ID NO 17122
LENGTH: 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 NRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 MAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTREAA 243
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llarity 41.0%; Pred. No. 1.8e-35;
Conservative 53; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                ; Score 535.5; DB 4;
; Pred. No. 4e-37;
69; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 38-10 (52052) B. CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Desulfitobacterium hafniense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9838, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 38.5%;
Matches 115; Conservative 69
                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-10-369-493-17122
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SEQ ID NO 9838
LENGTH: 299
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Matches 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-369-493-9838
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NSGUENCE 16570

Sequence 16570, Application US/10369493

PUBLICANT: Cao, VOIGWELL

APPLICANT: HINKLE, Green C.

APPLICANT: HINKLE, Green C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Kianten SKRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION 192052) B

CURRENT APPLICATION UNMERR: US/10/369,493

CURRENT FILING DATE: 2003:02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 VGLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 VTKKKIDEIVELVGLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 YYIQADDIQALTR----EAAAFRKVKVDEAEGGIEL--SIQKDEVPDLIKHLTDSGVRL 280
                                                                                                                                                                                                  52 GHMSITAGEIAVCGVSVKENPEKAARHIGAIVENPE-LYKFLTGYQNLQQYAR---MTKG 107
                                                                                                                                                                                                                           62 TLLEPSSGEAKVLGLDVVKDAREIRKRINLVAEGERTLYWRLTAYENLRYFASIYYIPRR 121
                                                                                                                                                                                                                                                                                                           168 IREIRDYLRKLTREKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKR 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                    4 LLELKNVSKTIRGKKI------IEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIV 51
                                                                                                                                         3 VIEVRNLRK-LYPKKIPLPPRKVEWPEALKGITFRVKKGELFGLLGPNGAGKTTIKILT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGE
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                                                                             31;
                                    Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.5%; Score 485; DB 4; Length 221; 46.2%; Pred. No. 5.2e-33; tive 51; Mismatches 61; Indels
                                  ; Score 491.5; DB 4; Length 3; Pred. No. 2.4e-33; 78; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 REKGMAVIVSSHLLSEMELMCDRIALIQNGKL 211 : :::|||:||:||:|| |||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 16570
LENGTH: 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Bacillus thuringiensis US-10-369-493-16570
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                                        31.9%;
35.2%;
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                                    Query Match 31.9
Best Local Similarity 35.2
Matches 112; Conservative
US-10-369-493-1336
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Best Local S
Matches 98
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Good Younge:

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: DIANTS WITH IMPROVED PROPERTIES

CURRENT PEPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 1336
                                                                                                                                                                   Q
                                                        APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
PILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT PILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1297
LENGTH: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 LEGY-EIKIETKQPLPEL----EIPDIIRIEKTTENKAIIFAKSDIRESISEELAKKGI 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTRE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 KGMAVIVSSHLLSEMELMCDRIALIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTRE 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 GVSVKENFEKAARHIGAIVENPELYKFLTGYONLOOYA---RMTKGVTKKKIDEIVELVG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 LELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVC 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 32.0%; Score 493; DB 4; Best Local Similarity 36.4%; Pred. No. 1.7e-33; Matches 118; Conservative 67; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 AAAFRKVKVDEAEGGIELSIQKDEVPDLIK--
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Sequence 1297, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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ORGANISM: Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Pyrococcus horikoshii
US-10-369-493-1297
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                                                                                                                                           GENERAL INFORMATION:

Sequence 21602, Application US/10369493

Fublication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Can, Yongwei

APPLICANT: Gldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS

TITLE OF INVENTION OF THE SOURCE OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
30.7%; Score 473; DB 4; Length 305;
Best Local Similarity 35.3%; Pred. No. 8.5e-32;
Matches 107; Conservative 77; Mismatches 103; Indels 16;
180 QERNITILISSHILAEIEQLVDRIGIIHEGKL 211
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: ISHIKAWA, UUN
APPLICANT: ISHIKAWA, UUN
APPLICANT: SHIRAWA, HIROSHI
APPLICANT: SHIRAWA, HIROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: HATTORI, MAGAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPREBERE: 2002-05-29
CURRENT APPLICATION NUMBER: US/10/156,761
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US-10-369-493-21602
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FLK 299
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                                                                                                         RESULT 14
US-10-369-493-21602
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US-10-156-761-12401
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106 PRSARTVLPHIGALIEGPALYGFLSGRDNLLRYDAADPTADPRTRRTRVAATLDRVGLTA 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 KENFEKAARHIGAIVENPELYKFLTGYQNLQQY----ARMTKGVTKKKIDEIVELVGLKN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 RINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKGM 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 AAGKKAKAYSLGMKQRLGLAAALLQPRRLLVLDEPTNGLDPQGMREIRSLVRELASD-GT 224
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37.0%; Pred. No. 2.7e-31;
rive 54; Mismatches 114; Indels
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02 .
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12401
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45974, Ap 45974, Ap 45974, Ap 79452, Ap 2420, Ap 2420, Ap 2420, Ap 2720, Ap 2720, Ap 27352, Ap 73529, Ap 73529, Ap 85263, Ap 85263, Ap 85263, Ap 83584, Ap 8
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ALIGNMENTS

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64 CGVSVKENFEKAARHIGAIVENPELYKFLIGYQNLQQYARMTKGVTKKKIDEIVELVGLK 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
Sequence 3584, Application US/10471571A

Sequence 3584, Application US/10471571A

Publication No. US20060115490A1

GENERAL INFORMATION:

APPLICANT: CHIRON SpA

TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLBIC ACIDS

FILE REPERENCE: PO26927WO

CURRENT APPLICATION NUMBER: US/10/471,571A

CURRENT FILING DATE: 2003-09-12

PRIOR FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 5642

SEQ ID NO 3584

LENGTH: 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 NRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 26.7%; Score 411.5; DB 6; Length 231; Best Local Similarity 37.3%; Pred. No. 1.5e-21; Matches 84; Conservative 61; Mismatches 65; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 MAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRY 228
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; OTHER INFORMATION: hypothetical protein US-10-471-571A-3584
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Staphylococcus aureus
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US-10-471-571A-1354 ; Sequence 1354, Application US/10471571A

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US-11-289-102-341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 ALTREAAAFRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 KYLAE--HFQLQNVDKADGHLMINAQKN-YQVILKALSELDIYPKYIETRKSSLRDTYFN 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 GVSVKENFEKAARHIGAIVENPELYKFLIGYQNLQQYAR-MTKGVTKKKIDEIVELVGLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 NRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 LELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKLEHITKKYGSNVVLNDIDFDFDFGDSRIVGLIGKNGVKTTVMKVMNGNIIKFDGKVDI- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS FILE REFERENCE: PO26927W0
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2003-09-12
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 716
LENGTH: 232
Publication No. US20060115490A1
GENERAL INFORMATION:
APPLICANT: CHIRON SON
TITLE OF INVENTION: STARPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P026927W0
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT PILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR PILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 1354
LENGTH: 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.2%; Score 404.5; DB 6;
31.2%; Pred. No. 6e-21;
tive 76; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , LOCATION: (1). (232)
, OTHER INFORMATION: hypothetical protein
US-10-471-571A-716
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MISC FEATURE
LOCATION: (1). (290)
OTHER INFORMATION: hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 716, Application US/10471571A Publication No. US20060115490A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                          ORGANISM: Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 VLAGHSVAR--EPSAAHLSMGYCPQSDAIFELLTGREHLELLARL-RGVPEAQVAQTAGS 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 GVSVKENFEKAARHIGAIVENPELYKFLTGYONLOOYARMTKGVTKKKIDEIVELVGLKN 124
                                                                                                                                                             S LELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVC 64
                                                                                         6 LVTENISKRFKNODVLKHINITLENNEVYGLLGINGAGKTTLMKIICGILQQDSGEIKLD 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 PARDEKKRYYIQADDTQALTREAAAFRKVKVDEAEGGIELSIQKDEVP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 -VELVGLKNRINDKVKTYSLGMRORLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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          Length 232;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 RKLTREKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDI---QHVHG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
22.7%; Score 349.5; DB 7; Length 5
Best Local Similarity 30.2%; Pred. No. 9e-17;
Matches 101; Conservative 68; Mismatches 108; Indels
                                        Indels
          Score 392.5; DB 6;
Pred. No. 3e-20;
5; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLIKHLTDSGVRLYEVKAVNKSLEDRFLEITADK 301
25.5%; Scor.
38.0%; Pred. No. oc.
444 55; Mismatches
                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-11-293.697-4274
i Sequence 4274, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TILE OF INVENTION: Novel full length CDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; RAIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SEQ ID NO 4274
                                                                                                                                                                                                                                                                                        185 AVIVSSHLLSEMELMCDRIAIIONGKLR 212
             Query Match 25.5%
Best Local Similarity 38.0%
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-11-293-697-4274
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119 DITENRKKRIDSLSKGNQQKIQLLASMLHKPELLILDEPFSGLDPVNVELLKEAVKDL-N 177
                                                                                                                                                                                                              65 GVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIV----ELV 120
                                                                                                                                                                                                                                                                                                                                                                                                  181 EKGMAVIVSSHLLSEMELMCDRIAIIQNGKL---RDIQHVHGPARDEKKRYYIQADDT-Q 236
                                                                                                                                                                                                                                                                                                                                                                                                                             : | | : : | | | : : | : | : | : | DWGSTIVYSSHRMEHVEELCODVCILDKGQLVVSGDINHVR--ASNGNKKVVIESETTLP 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 DLTWIRGI---IHSENMKQGLQLTIENEDVAKDIYQVVAHQGYVKRFQV--VEPSLQDIF 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 VCGVSVKENFEKAARHIGAIVENPELYKPLTGYQNLQQYARMTKGVTKKKIDEIV-ELVG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLTREKGMAVIVSSHLLSEMELMCDRIALIQNGKLRDIQHVHGPARDEKKR---YYIQA- 232
                                                                                                                     5 LELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: National institute of Agrobiological Sciences.
APPLICANT: National institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
ITLE REFERENCE: MOA-A02051-US
FILE REFERENCE: MOA-A02051-US
CURRENT APPLICATION NUMBER: UP 2002-203269
PRIOR PILING DATE: 2003-05-20
PRIOR PLING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: UP 2002-383870
PRIOR PLING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
                                                                                                                                                3 LVIEHVTKRFGKMTAVNDISLKLESGKMLGFLGRNGAGKTTTFRMILGLSEPTEGHITYN
                                                                                                                                                                                                                                         63 G---KKLDKTWYNRIGYLPEERGLHGKLTVEEEL-KYLATLKGMSKTEIOQOISYWLERP
                                                                                                                                                                                                                                                                                                          121 GLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 ALTREAAAFRKVKVDEAEGGIELSIQKDEV-PDLIKHLTDSG-VRLYEVKAVNKSLEDRF
                          Length 299
                        21.9%; Score 338; DB 6; Length 29
30.5%; Pred. No. 2.5e-16;
tive 70; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.5%; Score 331.5; DB 6;
29.4%; Pred. No. 3.2e-15;
tive 75; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 43324, Application US/10449902; Publication No. US20060123505A1; GENERAL INFORMATION:
                                                                          94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 29.44
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : | |:
291 IEKVGGKD 298
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US-10-449-902-43324
                        Query Match
Best Local Similarity
Matches 94; Conserv
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LENGTH: 949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 AGEIAVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 YLRKLTREKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDI----QHVHGP-ARDEKKRYY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 IQADDTQALTREAAAF-----RKVKVDEAEG-----GIELSIQKDEVPDLIKHLTDS 276
                                                              APPLICANT: Lee, Hyerim
APPLICANT: Lee, Hyerim
APPLICANT: Shaw, Peter M.
APPLICANT: Shaw, Peter M.
APPLICANT: Clark, Edwin
TITLE OF INVENTION: BIOWARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
TITLE OF INVENTION: MICROTUBULE-STABILIZING AGENTS
FILE REPERBRENCE: 10338 NP
CURRENT APPLICATION NUMBER: US/11/289,102
CURRENT FILING DATE: 2005-11-29
PRIOR PLILING DATE: 2005-11-39
PRIOR PLILING DATE: 2005-11-30
NUMBER OF SEQ ID NOS: 395
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LETLLELKNVSKTIRGK---KIIEGLSFDVRACEIFGFLGPNGAGKTTTIRMIVGHMSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 31; Gaps
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Publication No. US20060115490A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REPERENCE: POS6927W0
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT PILING DATE: 2003-09-12
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEC ID NOS: 5642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 346.5; DB 7;
; Pred. No. 6.2e-16;
58; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1). (299)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-4370
Sequence 341, Application US/11289102
Publication No. US20060121511A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1673 YGVDDYSVSQI--SLEQVFL 1690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GVRLYEVKAVNKSLEDRFL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 4370
LENGTH: 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 32.8%
Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MISC_FEATURE
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                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 341
LENGTH: 1704
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Indels

Length 949;

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180 REKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHG--------PAR 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 VGLKARINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 WGLSDKADTAYGSLSGGQQQRLSIALALVGKPRIAVFDELTTALDPHARRETWKLIEKV- 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 CGVSVKENFEKA--ARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKID--EIVEL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 54801, Application US/10449902

| Sequence 54801, Application US/10449902
| Publication No. US2006012350341
| GENERAL INFORMATION:
| APPLICANT: National Institute of Agrobiological Sciences.
| APPLICANT: The Institute of Physical and Chemical Research, APPLICANT: The Institute of Physical and Chemical Research.
| APPLICANT: The Institute of Physical and Chemical Research.
| APPLICANT: The Institute of Physical and Chemical Research.
| APPLICANT: The Institute of Physical and Chemical Research.
| TITLE OF INVENTION: FOLL-LENGTH PLANT CDNA AND USES THEREOF.
| TITLE OF ILING DATE: 2002-05-29
| CURRENT TILING DATE: 2002-05-30
| PRIOR FILING DATE: 2002-05-30
| PRIOR FILING DATE: 2002-12-11
| NUMBER OF SEQ ID NOS: 56791
| SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                             4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV
                                                                                                                                                                                                                                                                                                    Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.5%; Score 315.5; DB 6; Length 968; 36.3%; Pred. No. 4.1e-14;
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.1e-14;
76;
                                                                                                                                                                                                                                                                                                    th 20.5%; Score 316.5; DB 7; Similarity 27.9%; Pred. No. 7.8e-15; 89; Conservative 64; Mismatches 125;
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FILE REFERENCE: 1855/256
CURRENT APPLICATION NUMBER: US/11/274,683
CURRENT FILING DATE: 2005-11-14
PRIOR APPLICATION NUMBER: US 60/627,752
PRIOR FILING DATE: 2004-11-12
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.3
SOFTWARE: Patentin version 3.3
LENGTH: 304
                                                                                                                                                                                                                                   ORGANISM: Streptomyces sp. NRRL 30748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 VKAVNKSLEDRFLEITADK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :: ||:| |: | |
283 LRLEQASLDDAFVALTGSK 301
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                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 89; Conserv
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Matches 73; Conser
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US-10-449-902-54801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 KLTREKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKR---YYIQA- 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----DDTQALTREAAA-FRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               864 TISPEFEGEVENLARKLSPNARKVYHLSGTOKYELPKÖQVRIADVFM-AVENFKRTEVO 922
                                                                                    864 TISPEFEQEVENLARKLSPNARKVYHLSGTQKYELPKQQVRIADVFM-AVENFKRRTEVQ 922
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       810 QAKRDR--AIVLTTHSMEEAEVLCDRLCIMVDGSLQCI----GTPKELIARYGGYYVLTM 863
                                                  -----DDTQALTREAAA-FRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVK 284
                                                                                                                                                                                                                                                                                               Sequence 44552, Application US/10449902

Sequence 44552, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

ITLE REFERENCE: MOA-A0205Y1-US

FULE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT FILING DATE: 2003-05-29

PRIOR PLING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: UF 2002-183870

PRIOR PLING DATE: 2002-15-11

NUMBER OF SEQ ID NOS: 56791

SEQ ID NO 44592

LENGTH: 949

LENGTH: 949
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APPLICANT: Haltli, Bradley A
TITLE OF INVENTION: Elaiophylin biosynthetic gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.5%; Score 331.5; DB 6; 29.4%; Pred. No. 3.2e-15; tive 75; Mismatches 120;
                                                                                                                                                                         923 AWGLADTTMEDVFVKVAKGAQSSEEL 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 A---VNKSLEDRFLEITADKEEAQHV 307
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                                                                                                                                              285 A---VNKSLEDRFLEITADKEEAQHV 307
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. Sequence 30, Application US/11274683
. Publication No. US20060141583A1
. GENERAL INFORMATION:
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US-10-449-902-44592
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Best Local Similarity
Matches 96, Conserva
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138 RQRLGLAQSLLHDPKLLILDBPTNGLDPAGIREIRDYLRKLTREKGMAVIVSSHLLSEME 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 KVDEAEGGIELSIOKDEVP-DLIKHLTDSGVRLYEVK---AVNK-----SLEDRFLEIT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 CGVSVKENFEKAAR-HIGAIVENPELYKFLTGYQNLQQYARMTKGVTK----KKIDEIVEL 119
                                                                                                                                                                                                                                                                                                                                                36 ISFCVKKGEILGLLGPNGAGKSTIINILVGDIEPTSGQVFLGDYSSETSEDDDSLKCMGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VIKFKAVTKRYGKHVAVDNISFNINEGEFFVLIGPSGCGKTTTLKMINRLIHLSEGYIYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :::| | |:| :::| | |:| 355 KRKLCFALSMLGNPQITLLDEPSTGMDPKAKQHMWRAIRTAFKNRKRAAILTTHYMERAE
                                                                                                                                                                                                                                                                                                                      23 LSPDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVCGVSVK-ENFEKAARHIGA
                                                                                                                                                                                                                                                                                                                                                                                                          82 IVENPELYKFLIGYQNLQQYARMTKGVT----KKKIDEIVELVGLKARINDKVKTYSLGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3086, Application US/10471571A

Publication No. US20060115490A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
TITLE REFERENCE: P026927WO
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
FRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 3086
                                                                                                                                                                                                                                                                              29;
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                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                  19.7%; Score 303.5; DB 7;
28.9%; Pred. No. 1.4e-13;
tive 73; Mismatches 115;
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CTHER INFORMATION: hypothetical protein
US-10-471-571A-3086
  CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2603
                                                                                                                                                                                                                                                                              88; Conservative
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                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-2603
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                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 88; Conserval
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                                                                                                                               LENGTH: 559
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                                       78 HIGAIVENPELYKFLIGYQNLQQYARMTKGVTKKKIDEIVE----LVGLKNRINDKVKTY 133
                                                                                                                                                   134 SLGMRORLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKGMAVIVSSHLL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 549 VKGLWVNLEXDQLFCLLGPNGAGKTTTISCLTGITPITGGDAMIYGHSVRSTAGMSNIRR 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 KAARHIGAIVENPELYKFLTGYONLOOYARMTKGVTKK----KIDEIVELVGLKNRINDK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 SHLLSEMELMCDRIAIIQNGKLR---DIQHVHGPARDEKKRYYI---QADDTQALTRBAA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 AFRKVKVDEA--EGGIELSIQKDEVPDL-----IKHLTDSGVRLYEVKAVNKS 289
                                                                               609 MIGVCPQFDILWDALTAKEHMELFASI-KGLPPSTIKSVAEQSLIQVKLSQAANVRAGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGKKI-IEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVCGVSVKENFE
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                                                                                                                                                                                                                                                                                                                                                       Sequence 4238, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A01106
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR FILING DATE: 2005-12-05
PRIOR FILING DATE: 2005-12-05
SOFTWARE: PALENTIN NOVER: 215
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Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A01106
CURRENT APPLICATION NUMBER: US/11/293,697
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780 LEKVFLELSKEQE 792
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Best Local Similarity 30.7*
Matches 96; Conservative
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LENGTH: 815
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                                                                         231
                                                                                                                                             EIAVCGVSV----KENFEKAARHIGAIVENPELYKFLTGYQNLQ----OYARMTKGVTKKK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ALELVELVGLKGREKAYPSELSGGQKQRVGIARALANDPTVLLCDEATSALDPQTTDEIL 180
                                                     VGL----KONRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDY 174
                                                                                                                                                                                                --ADDTQALTREAAAFRKV----KVDEAEGGIELSIQKDEVP-DLIKHLTDSGVRLYEVK 284
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2868, Application US/10471571A

Publication No. US20060115490A1

GENERAL INFORMATION:

APPLICANT: CHIRON SPA

TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REPERENCE: P026927W0

CURRENT FILING DATE: 2003-09-12

PRIOR APPLICATION NUMBER: US/10/471,571A

CURRENT FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-7

NUMBER OF SEQ ID NOS: 564-27

SOFTWARE: SEGWIN99, version 1.03
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LOCATION: (1)..(341)

OTHER INFORMATION: ABC transporter ATP-binding
US-10-471-571A-2868
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                                                                                                                                                                                                                                                                                          EDSVGQYVIDRKDIFKYLSQKKEVAQH 324
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US-10-471-571A-2868
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US-10-471-571A-678
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APPLICANT: CHIRON SPA TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS FILE REFERENCE: P026927WO

Sequence 678, Application US/10471571A Publication No. US20060115490A1 GENERAL INFORMATION:

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75 AARHIGAIVENPELYKFLTGYQNLQQYARMT-----KGVTKKKIDEIVELVGLKNRIN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 DKVKTYSLGMRORLGLAOSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKGMAVI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 GKK-IIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVCGVSVKENFEK 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 VSSHLLSEMELMCDRIAIIQNGK-----LRDIQHVHGPARDEKKRYYIQADDTQA 237
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Best Local Similarity 28.5%; Pred. No. 2.2e-13;
Matches 68; Conservative 62; Mismatches 87; Indels
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 678
                                                                                                                                                                                                                                                                 ; LOCATION: (1). 7(256)
; OTHER INFORMATION: ABC transporter ecsA US-10-471-571A-678
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